

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :

C12N 15/31, 15/62, C07K 14/295, 16/12,
19/00, A01K 67/027, A61K 39/118,
G01N 33/53, C12Q 1/68

A2

(11) International Publication Number:

WO 99/27105

(43) International Publication Date:

3 June 1999 (03.06.99)

(21) International Application Number: PCT/IB98/01890

(22) International Filing Date: 20 November 1998 (20.11.98)

(30) Priority Data:

97/14673	21 November 1997 (21.11.97)	FR
60/107,078	4 November 1998 (04.11.98)	US

(71) Applicant (for all designated States except US): GENSET
[FR/FR]; 24, rue Royale, F-75008 Paris (FR).

(72) Inventor; and:

(75) Inventor/Applicant (for US only): GRIFFAIS, Rémy [FR/FR];
51, boulevard Romain Roland, F-92120 Montrouge (FR).(74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau,
26, avenue Kléber, F-75116 Paris (FR).(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR,
BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE,
GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ,
LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW,
MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL,
TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO
patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR,
IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished
upon receipt of that report.(54) Title: *CHLAMYDIA PNEUMONIAE* GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES
THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION

(57) Abstract

The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of *Chlamydia pneumoniae*, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

CHLAMYDIA PNEUMONIAE GENOMIC SEQUENCE AND POLYPEPTIDES,
FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS,
PREVENTION AND TREATMENT OF INFECTION

5

The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of *Chlamydia pneumoniae*, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection.

10 The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

20 Comparative analysis of the sequence of the gene encoding the ribosomal 16S RNA has been widely used for the phylogenetic study of prokaryotes. This approach has made it possible to classify the Chlamydiae among the eubacteria, among which they represent a well-isolated group, with, nevertheless, a very weak link with the planctomyces. The Chlamydiae thus exhibit some unique characteristics within the eubacteria, in particular their development cycle and the structure of their membranes. They have a unique two-phase cell cycle: the elementary body, a small extracellular form, attaches to the host and is phagocytosed; in the phagosome, it is converted to the replicative intracellular form, the reticulate body. The Chlamydiae are obligate intracellular bacteria which multiply in eukaryotic cells at the expense of their energy reserves and nucleotide pools; they are responsible for a wide variety of diseases in mammals and birds. The Chlamydiae are the only members of the order Chlamydiales, of the family Chlamydiaceae and of the genus *Chlamydia*. Within the genus *Chlamydia*, four species are currently described: *Chlamydia trachomatis*, *Chlamydia psittaci*, *Chlamydia pneumoniae* and *Chlamydia pecorum*. These bacteria are grouped together and share biological and biochemical properties. Among them, only the first three infect humans, *Chlamydia pecorum* being a pathogen of ruminants.

35 The species *Chlamydia psittaci* infects many animals, in particular birds, and is transmissible to humans. It is responsible for atypical pneumonia, for hepatic and renal dysfunction, for endocarditis and for conjunctivitis.

The species *Chlamydia trachomatis* is the best characterized. Besides a murine strain, it is divided into two groups which are distinguishable by the nature of the diseases for which they are responsible: trachoma, genital attack and venereal lymphogranulomatosis. There are fifteen human serotypes of *Chlamydia trachomatis* (A, K) and LGV (L1, L2, L3). Strains A to C are mainly found in eye infections, whereas strains D to K and LGV are essentially responsible for genital entry infections. It should be mentioned that the LGV strains are responsible for systemic diseases. Historically, it was in 1906 that Halberstaeder and Von Provaseck discovered, in trachoma patients, the presence of inclusions in the cytoplasm of the cells derived from conjunctival scrapings. In 1940, Rake and Jones described these same inclusions in certain cells obtained by puncturing the ganglia from a patient suffering from venereal granulomatosis. Characterization of the *Chlamydia trachomatis* microorganism was only successfully carried out in 1957, after a series of isolations in cell cultures.

It was in 1983 that *Chlamydia pneumoniae* was recognized as a human pathogen (Grayston JT et al., 1986); since then, special attention has been paid to this bacterium and it is estimated (Gaydos CA et al., 1994) that 10% of pneumonias, and 5% of bronchitides and sinusites are attributable to *Chlamydia pneumoniae* (Aldous MB et al., 1992). More recently, the association of this bacterium with the pathogenesis of asthmatic disease and of cardiovascular impairments is increasingly of interest.

Serological studies have made it possible to observe that *Chlamydia pneumoniae* infection is common in children between 5 and 16 years of age. Before this age, it is rare to find antibodies; the increase in the number of individuals carrying antibodies is then correlated with age up to 20 years. Accordingly, 50% of adults are carriers of antibodies, it being possible for this prevalence to be as high as 75%. These figures are all the more striking since a first infection induces antibody levels of which the persistence over time is limited to 3 or at most 5 years, which suggests frequent reinfection during the entire lifespan. The annual seroconversion rate is about 8% between 8 and 12 years and about 6% between 12 and 16 years (Haidl et al., 1994). Before the age of 15 years, the seroprevalence of the disease is identical between both sexes. After this age, men are more frequently infected than women; this is true in all regions worldwide where such studies have been carried out.

These infections are geographically highly widespread, as shown by numerous studies carried out throughout the world (Kanamoto Y et al., 1991; Tong CY et al., 1993). Developed countries of the north such as Canada, Denmark and Norway have the lowest infection rates; conversely, the highest prevalence rates are found in the less developed countries of tropical regions where the infection may occur before the age of 5 years.

Humans are the only known reservoir for *Chlamydia pneumoniae* and it is probable that the infection is caused by direct transmission, respiratory secretions probably being responsible for this low-yield transmission (Aldous et al., 1992). The chain of transmission may also appear to be indirect (Kleemola M et al., 1988), suggesting that the infection is caused by an effective transmission, but also that asymptomatic carriers exist, which could explain the high prevalence of the disease.

Other studies (Mordhorst CH et al., 1992) show that the efficiency of the transmission varies according to the individuals and list cases of infection affecting all or the majority of members of one family or of a group of families. The period of incubation is several weeks, significantly longer in this regard than that of many other respiratory pathogenic agents. Although under conditions of high
5 relative humidity the infectivity of *Chlamydia pneumoniae* in the open air decreases rapidly, suggesting a direct mode of transmission under these conditions, it is probable that the transmission occurs in some cases indirectly since the microorganism can survive for up to 30 hours in a hostile environment (Falsey et al., 1993).

Clinical manifestations due to *Chlamydia pneumoniae* are essentially respiratory
10 diseases. Pneumonia and bronchitis are the most frequent because they are clinically patent: since etiological diagnosis is evoked in this case, the infectious agent is identified. The asymptomatic diseases are probably numerous (Grayston JT et al., 1992; Grayston JT et al., 1986; Thom DH et al., 1990). The disease then progresses via bronchitis or pneumonia; fever is absent at the time of examination but is sometimes reported by the patient. The degree of seriousness of the disease is
15 variable and in hospitalized patients, it is common to observe pleural effusion; a generalized infection may also be observed and, in severe cases, anatomicopathological examination shows *Chlamydia pneumoniae* diseases.

Other syndromes such as sinusitis (Hashiguchi K et al., 1992), purulent otitis media (Ogawa H et al., 1992), or pharyngitis (Huovinen P et al., 1989) have been described, as well as
20 infections with respiratory impairments similar to asthma (Hahn DL et al., 1991). *Chlamydia pneumoniae* has also been associated with sarcoidosis, with erythema nodosum (Sundelof et al., 1993) and one case of Guillain-Barré syndrome has even been described (Haidl et al., 1992). The involvement of *Chlamydia pneumoniae* in Reiter's syndrome has also been evaluated (Braun J et al., 1994).

25 The association of *Chlamydia pneumoniae* with coronary diseases and with myocardial infarction was first suspected from the observation of the high antibody level in 71% of patients having a heart disease (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M et al., 1993; Thomas GN et al., 1997). Studies carried out in several countries have shown similar results in patients with atheromatous impairments (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M
30 et al., 1993; Grayston JT et al., 1996; Casas-Ciria J et al., 1996; Thomas GN et al., 1997; Jackson LA et al., 1997) and in patients with carotid impairments. Anatomicopathological and microbiological studies have detected *Chlamydia pneumoniae* in the vessels. The electron microscope has made it possible to visualize the bacterium (Ladany S et al., 1989), which has in fact been demonstrated by other techniques such as PCR (Campbell LA et al., 1992; Kuo CC et al., 1993; Kuo CC et al., 1988). It
35 also appears that the bacterium is more frequently found in old atheromatous lesions. Other studies carried out on young subjects from 15 to 35 years have given the opportunity to study the coronary arteries of people without atherosclerosis, this observation not being possible in older subjects (the

onset of the atheromatous disease is early). In these young subjects, the PCR studies did not find *Chlamydia pneumoniae* in subjects free of atheromatous disease, but revealed the presence of *Chlamydia pneumoniae* in two of the eleven subjects who showed early lesions and in six of the seven subjects who developed atheroma plaques. These studies therefore show that the atheroma plaque is
5 very strongly correlated with the presence of *Chlamydia pneumoniae*, but the role played by the bacterium in vascular pathology is not yet defined.

The data relating to controlled clinical studies analysing the effect of treatments in *Chlamydia pneumoniae* infections are limited in number. Unlike penicillin, ampicillin or the sulphamides, erythromycin, tetracycline or doxycycline show an antibiotic activity *in vitro* against
10 *Chlamydia pneumoniae*. However, a treatment at high doses should be continued for several weeks in order to avoid a recurrence of the infection. Accordingly, the use of two new macrolides, clarithromycin and azithromycin, whose diffusion, bioavailability and half-life allow shorter and better tolerated cures, is nowadays preferred. In the absence of definitive proof based on the results of clinical studies, an effective, without recurrences, and well-tolerated treatment of *Chlamydia*
15 *pneumoniae* infections therefore remains desirable.

An even more important need up until now relates to a specific and sensitive diagnosis, which can be carried out conveniently and rapidly, allowing early screening for the infection. Methods based on *Chlamydia pneumoniae* culture are slow and require a considerable know-how because of the difficulty involved in the collection, preservation and storage of the strain under appropriate
20 conditions. Methods based on antigen detection (EIA, DFA) or on nucleic acid amplification (PCR) provide tests which are more suitable for laboratory practice. A reliable, sensitive and convenient test, which allows distinction between serogroups and a fortiori between *Chlamydia pneumoniae* species is therefore highly desirable.

This is all the more important since the symptoms of *Chlamydia pneumoniae* infection
25 appear slowly, since all the pathologies associated with these infections have not yet been identified, and since, as has been mentioned above, an association is suspected between these infections and serious chronic infections, asthma or atherosclerosis.

No vaccine is yet available against *Chlamydia pneumoniae*: this is due to the labile nature of the antigens specific to the strain, which has so far prevented their specific identification.

30 Although the number of studies and of animal models developed is high, the antigens used have not induced sufficient protective immunity to lead to the development of human vaccines. In the case of *Chlamydia pneumoniae*, the role of the immune defense in the physiology and pathology of the disease should probably be understood in order to develop satisfactory vaccines.

More detailed information relating to the biology of these strains, their interactions with
35 their hosts, the associated phenomena of infectivity and those of escaping the immune defenses of the host in particular, and finally their involvement in the development of the these associated pathologies, will allow a better understanding of these mechanisms. In the light of the preceding text which shows

in particular the limitations of the means of controlling *Chlamydia pneumoniae* infection, it is therefore at present essential, on the one hand, to develop molecular tools, in particular from a better genetic knowledge of *Chlamydia pneumoniae*, but also to develop new preventive and therapeutic treatments, new diagnostic methods and new vaccine strategies which are specific, effective and
5 tolerated. This is precisely the object of the present invention.

The subject of the present invention is the nucleotide sequence having the sequence SEQ ID No. 1 of the *Chlamydia pneumoniae* genome. However, the invention is not limited to SEQ ID No. 1, but encompasses genomes and nucleotides encoding polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

10 Thus, the subject of the present invention encompasses nucleotide sequences characterized in that they are chosen from:

- a) the nucleotide sequence of SEQ ID No. 1, a nucleotide sequence exhibiting at least 99.9% identity with the sequence SEQ ID No. 1, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. ____, the nucleotide sequence of a clone insert
15 within ATCC Deposit No. __;
- b) a nucleotide sequence homologous to the sequence SEQ ID No. 1;
- c) a polynucleotide sequence that hybridizes to the nucleotide sequence of a) under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are
20 as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Alternatively, the hybridization step
25 can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following
30 the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

35 (ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a

temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

- d) a nucleotide sequence complementary to the sequence SEQ ID No. 1 or complementary to a nucleotide sequence as defined in a), b) or c) and a nucleotide sequence of their corresponding RNA;
- e) a nucleotide sequence of a representative fragment of the sequence SEQ ID No. 1, or of a representative fragment of the nucleotide sequence as defined in a), b), c) or d);
- f) a nucleotide sequence comprising a sequence as defined in a), b), c), d) or e);
- g) a nucleotide sequence capable of being obtained from a nucleotide sequence as defined in a), b), c), d), e) or f); and
- h) a modified nucleotide sequence of a nucleotide sequence as defined in a), b), c), d), e), f) or g).

Nucleotide sequence, polynucleotide or nucleic acid are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of transcription of the said DNAs.

It should be understood that the present invention does not relate to the genomic nucleotide sequences of *Chlamydia pneumoniae* taken in their natural environment, that is to say in the natural state. They are sequences which may have been isolated, purified or partially purified, by separation methods such as, for example, ion-exchange chromatography, molecular size exclusion chromatography or affinity chromatography, or alternatively fractionation techniques based on solubility in various solvents, or by genetic engineering methods such as amplification, cloning or subcloning, it being possible for the sequences of the invention to be carried by vectors.

The nucleotide sequence SEQ ID No. 1 was obtained by sequencing the *Chlamydia pneumoniae* genome by the method of directed sequencing after fluorescent automated sequencing of the inserts of clones and assembling of these sequences of nucleotide fragments (inserts) by means of softwares (cf. Examples). In spite of the high precision of the sequence SEQ ID No. 1, it is possible that it does not perfectly, 100% represent the nucleotide sequence of the *Chlamydia pneumoniae* genome and that a few rare sequencing errors or uncertainties still remain in the sequence SEQ ID No. 1. In the present invention, the presence of an uncertainty for an amino acid is designated by "Xaa" and that for a nucleotide is designated by "N" in the sequence listing below. These few rare errors or uncertainties could be easily detected and corrected by persons skilled in the art using the entire chromosome and/or its representative fragments according to the invention and standard

amplification, cloning and sequencing methods, it being possible for the sequences obtained to be easily compared, in particular by means of a computer software and using computer-readable media for recording the sequences according to the invention as described, for example, below. After correcting these possible rare errors or uncertainties, the corrected nucleotide sequence obtained would still exhibit at least 99.9% identity with the sequence SEQ ID No. 1. Such rare sequencing uncertainties are not present within the DNA contained within ATCC Deposit No. ___ or ___, and whatever rare sequence uncertainties that exist within SEQ ID No. 1 can routinely be corrected utilizing the DNA of the ATCC deposits.

Homologous nucleotide sequence for the purposes of the present invention is understood to mean a nucleotide sequence having a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, this percentage being purely statistical and it being possible for the differences between the two nucleotide sequences to be distributed randomly and over their entire length. The said homologous sequences exhibiting a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, may comprise, for example, the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the Chlamydia family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. In the present invention, the terms family and genus are mutually interchangeable, the terms variant, serotype, strain and subspecies are also mutually interchangeable. These homologous sequences may thus correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85(8):2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol.* 215(3):403-410; Thompson *et al.*, 1994, *Nucleic Acids Res.* 22(2):4673-4680; Higgins *et al.*, 1996, *Methods Enzymol.* 266:383-402; Altschul *et al.*, 1990, *J. Mol. Biol.* 215(3):403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272; Altschul *et al.*, 1997,

Nuc. Acids Res. 25:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

- (1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- 5 (2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3)BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4)TBLASTN compares a query protein sequence against a nucleotide sequence database
- 10 translated in all six reading frames (both strands); and
- (5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science* 256:1443-1445; Henikoff and Henikoff, 1993, *Proteins* 17:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 20 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, 25 Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268).

Nucleotide sequence complementary to a sequence of the invention is understood to mean any DNA whose nucleotides are complementary to those of the sequence of the invention, and whose orientation is reversed (antiparallel sequence).

30 The present invention further comprises fragments of the sequences of a) through f), above. Representative fragments of the sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. It is understood that such fragments refer only to portions of SEQ ID No. 1 that are not currently listed in a publicly available database.

Among these representative fragments, those capable of hybridizing under stringent conditions with a nucleotide sequence according to the invention are preferred. Hybridization under

stringent conditions means that the temperature and ionic strength conditions are chosen such that they allow hybridization to be maintained between two complementary DNA fragments.

By way of illustration, high stringency conditions for the hybridization step for the purposes of defining the nucleotide fragments described above, are advantageously the following.

5 The hybridization is carried out at a preferred temperature of 65EC in the presence of SSC buffer, 1 × SSC corresponding to 0.15 M NaCl and 0.05 M Na citrate. The washing steps may be, for example, the following:

2 × SSC, 0.1% SDS at room temperature followed by three washes with 1 × SSC, 0.1% SDS; 0.5 × SSC, 0.1% SDS; 0.1 × SSC, 0.1% SDS at 68EC for 15 minutes.

10 Intermediate stringency conditions, using, for example, a temperature of 60EC in the presence of a 5 × SSC buffer, or of low stringency, for example a temperature of 50EC in the presence of a 5 × SSC buffer, respectively require a lower overall complementarity for the hybridization between the two sequences.

 The stringent hybridization conditions described above for a polynucleotide of about
15 300 bases in size will be adapted by persons skilled in the art for larger- or smaller-sized oligonucleotides, according to the teaching of Sambrook et al., 1989.

 Among the representative fragments according to the invention, those which can be used as primer or probe in methods which make it possible to obtain homologous sequences or their representative fragments according to the invention, or to reconstitute a genomic fragment found to be
20 incomplete in the sequence SEQ ID No. 1 or carrying an error or an uncertainty, are also preferred, these methods, such as the polymerase chain reaction (PCR), cloning and sequencing of nucleic acid being well known to persons skilled in the art. These homologous nucleotide sequences corresponding to mutations or to inter- or intra-species variations, as well as the complete genomic sequence or one of its representative fragments capable of being reconstituted, of course form part of
25 the invention.

 Among the said representative fragments, those which can be used as primer or probe in methods allowing diagnosis of the presence of *Chlamydia pneumoniae* or one of its associated microorganisms as defined below are also preferred.

 The representative fragments capable of modulating, regulating, inhibiting or inducing
30 the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the host cell and/or organism, are also preferred. Replication cycle is intended to designate invasion, multiplication, intracellular localization, in particular retention in the vacuole and inhibition of the process of fusion to the lysosome, and propagation of *Chlamydia pneumoniae* or one
35 of its associated microorganisms from host cells to host cells.

 Among the said representative fragments, those corresponding to nucleotide sequences corresponding to open reading frames, called ORF sequences (ORF for open reading frame), and

encoding polypeptides, such as for example, but without being limited thereto, the ORF sequences which will be later described, are finally preferred.

The representative fragments according to the invention may be obtained, for example, by specific amplification, such as PCR, or after digestion, with appropriate restriction enzymes, of nucleotide sequences according to the invention; these methods are in particular described in the manual by Sambrook et al., 1989. The said representative fragments may also be obtained by chemical synthesis when they are not too large in size and according to methods well known to persons skilled in the art. For example, such fragments can be obtained by isolating fragments of the genomic DNA of ATCC Deposit No. ____ or a clone insert present at this ATCC Deposit No. ____.

10 The representative fragments according to the invention may be used, for example, as primer, to reconstitute some of the said representative fragments, in particular those in which a portion of the sequence is likely to be missing or imperfect, by methods well known to persons skilled in the art such as amplification, cloning or sequencing techniques.

Modified nucleotide sequence will be understood to mean any nucleotide sequence obtained by mutagenesis according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the normal sequences, for example mutations in the regulatory and/or promoter sequences for the expression of a polypeptide, in particular leading to a modification of the level of expression of the said polypeptide or to a modulation of the replicative cycle.

Modified nucleotide sequence will also be understood to mean any nucleotide sequence encoding a modified polypeptide as defined below.

The subject of the present invention also includes *Chlamydia pneumoniae* nucleotide sequences characterized in that they are chosen from a nucleotide sequence of an open reading frame (ORF), that is, the ORF2 to ORF1297 sequences.

The ORF2 to ORF1297 nucleotide sequences are defined in Tables 1 and 2, *infra*, by their position on the sequence SEQ ID No. 1. For example, the ORF2 sequence is defined by the nucleotide sequence between the nucleotides at position 42 and 794 on the sequence SEQ ID No. 1, ends included. ORF2 to ORF1297 have been identified via homology analyses as well as via analyses of potential ORF start sites, as discussed in the examples below. It is to be understood that each identified ORF of the invention comprises a nucleotide sequence that spans the contiguous nucleotide sequence from the ORF stop codon immediately 3' to the stop codon of the preceding ORF and through the 5' codon to the next stop codon of SEQ ID No.:1 in-frame to the ORF nucleotide sequence. Table 2, *infra*, lists the beginning, end and potential start site of each of ORFs 1-1297. In one embodiment, the ORF comprises the contiguous nucleotide sequence spanning from the potential ORF start site downstream (that is, 3') to the ORF stop codon (or the ORF codon immediately adjacent to and upstream of the ORF stop codon). ORF2 to ORF1297 encode the polypeptides of SEQ ID No. 2 to SEQ ID No. 1291 and of SEQ ID No. 6844 to SEQ ID No. 6849, respectively.

Upon introduction of minor frameshifts, certain individual ORFs can comprise larger

"combined" ORFs. A list of such putative "combined" ORFs is shown in Table 3, below. For example, a combined ORF can comprise ORF 25, ORF 26 and ORF 27, including intervening in-frame, nucleotide sequences. The order of ORFs (5' to 3'), within each "combined" ORF is as listed. It is to be understood that when ORF2 to ORF1297 are referred to herein, such reference is also meant to include "combined" ORFs. Polypeptide sequences encoded by such "combined" ORFs are also part of the present invention.

Table 3

	ORF 25, ORF 26, ORF 27;
10	ORF 28, ORF 29, ORF 30;
	ORF 31, ORF 32;
	ORF 33, ORF 35;
	ORF 466, ORF 467;
	ORF 468, ORF 469;
15	ORF 477, ORF 476, ORF 474;
	ORF 480, ORF 482;
	ORF 483, ORF 485, ORF 486, ORF 500;
	ORF 503, ORF 504, ORF 505;
	ORF 506, ORF 507;
20	ORF 1211, ORF 647;
	ORF 1286, ORF 1039;
	ORF 691, ORF 690;
	ORF 105, ORF 106;
	ORF 170, ORF 171; ORF 394, ORF 393;
25	ORF 453, ORF 452, ORF 451;
	ORF 526, ORF 525;
	ORF 757, ORF 756, ORF 755;
	ORF 856, ORF 855;
	ORF 958, ORF 957;
30	ORF 915, ORF 914, ORF 913;
	ORF 543, ORF 544;
	ORF 1266, ORF 380;
	ORF 745, ORF 744;
	ORF 777, ORF 776;
35	ORF 343, ORF 1297, and representative fragments.

Table 1 also depicts the results of homology searches that compared the sequences of the

polypeptides encoded by each of the ORFs to sequences present in public published databases. It is understood that those polypeptides listed in Table 1 as exhibiting greater than about 95% identity to a polypeptide present in a publicly disclosed database are not considered part of the present invention; likewise in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention. In another embodiment, it is understood that those polypeptides listed in Table 1 as exhibiting greater than about 99% identity to a polypeptide present in a publicly disclosed database are not considered part of the invention; likewise, in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention.

The invention also relates to the nucleotide sequences characterized in that they comprise a nucleotide sequence chosen from:

- a) an ORF2 to ORF1297, a "combined" ORF nucleotide sequence, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. _____ or the nucleotide sequence of a clone insert in ATCC Deposit No. _____ according to the invention;
- b) a homologous nucleotide sequence exhibiting at least 80% identity across an entire ORF2 to ORF1297 nucleotide sequence according to the invention or as defined in a);
- c) a polynucleotide sequence that hybridizes to ORF2 to ORF1297 under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate

stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

- d) complementary or RNA nucleotide sequence corresponding to an ORF2 to ORF1297 sequence according to the invention or as defined in a), b) or c);
- e) a nucleotide sequence of a representative fragment of an ORF2 to ORF1297 sequence according to the invention or of a sequence as defined in a), b), c) or d);
- 15 f) a nucleotide sequence capable of being obtained from an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d) or e); and
- g) a modified nucleotide sequence of an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d), e) or f);

As regards the homology with the ORF2 to ORF1297 nucleotide sequences, the homologous sequences exhibiting a percentage identity with the bases of one of the ORF2 to ORF1297 nucleotide sequences of at least 80%, preferably 90% and 95%, are preferred. Such homologous sequences are identified routinely via, for example, the algorithms described above and in the examples below. The said homologous sequences correspond to the homologous sequences as defined above and may comprise, for example, the sequences corresponding to the ORF sequences of a bacterium belonging to the *Chlamydia* family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the ORF sequences of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. These homologous sequences may likewise correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

The invention comprises polypeptides encoded by a nucleotide sequence according to the invention, preferably by a representative fragment of the sequence SEQ ID No. 1 and corresponding to an ORF sequence, in particular the *Chlamydia pneumoniae* polypeptides, characterized in that they are chosen from the sequences SEQ ID No. 2 to SEQ ID No. 1291 or SEQ ID No. 6844 to SEQ ID No.

6849 and representative fragments thereof. However, the invention is not limited to polypeptides encoded by ORFs in SEQ ID No. 1 and its corresponding ORF sequences, but encompasses polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the invention also comprises the polypeptides characterized in that they comprise a
5 polypeptide chosen from:

- a) a polypeptide encoded by a polynucleotide sequence in SEQ ID No. 1 (*e.g.*, any polypeptide encoded by a polynucleotide sequence corresponding to ORF2 to ORF1297 and/or representative fragments thereof) according to the invention;
- b) a polypeptide homologous to a polypeptide according to the invention, or as defined in a);
- 10 c) a polypeptide encoded by a polynucleotide sequence that hybridizes to SEQ ID No. 1 or ORF2 to ORF1297 under high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll,
15 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing
20 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989,
25 Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably such polypeptide represents a homolog of a polypeptide encoded by ORF2 to ORF1297. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such
30 sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are
35 detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual,

Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia*

5 *pneumoniae* polypeptide.

- d) a fragment of at least 5 amino acids of a polypeptide according to the invention, or as defined in a), b) or c);
- e) a biologically active fragment of a polypeptide according to the invention, or as defined in a), b), c) or d); and
- 10 f) a modified polypeptide of a polypeptide according to the invention, as defined in a), b), c), d) or e).

In the present description, the terms polypeptide, peptide and protein are interchangeable.

It should be understood that the invention does not relate to the polypeptides in natural form, that is to say that they are not taken in their natural environment but that they may have been
15 isolated or obtained by purification from natural sources, or alternatively obtained by genetic recombination, or else by chemical synthesis and that they may, in this case, comprise nonnatural amino acids, as will be described below.

Homologous polypeptide will be understood to designate the polypeptides exhibiting, in relation to the natural polypeptide, certain modifications such as in particular a deletion, addition or
20 substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, and/or a mutation, or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides, those whose amino acid sequence exhibits at least 80%, preferably 90%, homology or identity with the amino acid sequences of the polypeptides according to the invention are preferred. In the case of a substitution, one or more consecutive or nonconsecutive amino acids are replaced by "equivalent"
25 amino acids. The expression "equivalent" amino acid is intended here to designate any amino acid capable of being substituted for one of the amino acids in the basic structure without, however, essentially modifying the biological activities of the corresponding peptides and as will be defined later.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the
30 variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85(8):2444-2448; Altschul et al., 1990, *J. Mol. Biol.* 215(3):403-410; Thompson et al., 1994, *Nucleic Acids Res.* 22(2):4673-4680; Higgins et al., 1996, *Methods Enzymol.* 266:383-402; Altschul et al., 1990, *J. Mol. Biol.* 215(3):403-
35 410; Altschul et al., 1993, *Nature Genetics* 3:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see,

e.g., Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res.* 25:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

- 5 (1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
 - (2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
 - (3)BLASTX compares the six-frame conceptual translation products of a query
10 nucleotide sequence (both strands) against a protein sequence database;
 - (4)TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
 - (5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.
- 15 The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet
20 *et al.*, 1992, *Science* 256:1443-1445; Henikoff and Henikoff, 1993, *Proteins* 17:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment
25 pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268).

Equivalent amino acids may be determined either based on their structural homology
30 with the amino acids for which they are substituted, or on results of comparative tests of biological activity between the various polypeptides which may be carried out.

By way of example, there may be mentioned the possibilities of substitutions which may be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; the replacements, for example, of leucine with valine or
35 isoleucine, of aspartic acid with glutamic acid, of glutamine with asparagine, of arginine with lysine, and the like, the reverse substitutions naturally being feasible under the same conditions.

The homologous polypeptides also correspond to the polypeptides encoded by the

homologous nucleotide sequences as defined above and thus comprise in the present definition the mutated polypeptides or polypeptides corresponding to inter- or intra-species variations which may exist in *Chlamydia*, and which correspond in particular to truncations, substitutions, deletions and/or additions of at least one amino acid residue.

5 Biologically active fragment of a polypeptide according to the invention will be understood to designate in particular a polypeptide fragment, as defined below, exhibiting at least one of the characteristics of the polypeptides according to the invention, in particular in that it is:

- capable of eliciting an immune response directed against *Chlamydia pneumoniae*; and/or
- capable of being recognized by an antibody specific for a polypeptide according to the invention;
- 10 and/or
- capable of binding to a polypeptide or to a nucleotide sequence of *Chlamydia pneumoniae*; and/or
- capable of modulating, regulating, inducing or inhibiting the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the
- 15 host cell and/or organism; and/or
- capable of generally exerting an even partial physiological activity, such as for example a structural activity (cellular envelope, ribosome), an enzymatic (metabolic) activity, a transport activity, an activity in the secretion or in the virulence.

A polypeptide fragment according to the invention is understood to designate a
20 polypeptide comprising a minimum of 5 amino acids, preferably 10 amino acids or preferably 15 amino acids. It is to be understood that such fragments refer only to portions of polypeptides encoded by ORF2 to ORF1297 that are not currently listed in a publicly available database.

The polypeptide fragments according to the invention may correspond to isolated or purified fragments which are naturally present in *Chlamydia pneumoniae* or which are secreted by
25 *Chlamydia pneumoniae*, or may correspond to fragments capable of being obtained by cleaving the said polypeptide with a proteolytic enzyme, such as trypsin or chymotrypsin or collagenase, or with a chemical reagent, such as cyanogen bromide (CNBr) or alternatively by placing the said polypeptide in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by chemical synthesis, using hosts transformed with an expression vector according to
30 the invention containing a nucleic acid allowing the expression of the said fragments, placed under the control of appropriate elements for regulation and/or expression.

"Modified polypeptide" of a polypeptide according to the invention is understood to designate a polypeptide obtained by genetic recombination or by chemical synthesis as will be described below, exhibiting at least one modification in relation to the normal sequence. These
35 modifications may in particular affect amino acids responsible for a specificity or for the efficiency of the activity, or responsible for the structural conformation, for the charge or for the hydrophobicity, and for the capacity for multimerization and for membrane insertion of the polypeptide according to

the invention. It is thus possible to create polypeptides with an equivalent, an increased or a reduced activity, and with an equivalent, a narrower or a broader specificity. Among the modified polypeptides, there may be mentioned the polypeptides in which up to 5 amino acids may be modified, truncated at the N- or C-terminal end, or alternatively deleted, or else added.

- 5 As is indicated, the modifications of the polypeptide may have in particular the objective:
- of making it capable of modulating, regulating, inhibiting or inducing the expression of a gene of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms,
 - 10 in the host cell and/or organism,
 - of allowing its use in methods of biosynthesis or of biodegradation, or its incorporation into vaccine compositions,
 - of modifying its bioavailability as a compound for therapeutic use.

 The said modified polypeptides may also be used on any cell or microorganism for which

15 the said modified polypeptides will be capable of modulating, regulating, inhibiting or inducing gene expression, or of modulating the growth or the replication cycle of the said cell or of the said microorganism. The methods allowing demonstration of the said modulations on eukaryotic or prokaryotic cells are well known to persons skilled in the art. The said cells or microorganisms will be chosen, in particular, from tumour cells or infectious microorganisms and the said modified

20 polypeptides may be used for the prevention or treatment of pathologies linked to the presence of the said cells or of the said microorganisms. It is also clearly understood that the nucleotide sequences encoding the said modified polypeptides may be used for the said modulations, for example by the intermediacy of vectors according to the invention and which are described below, so as to prevent or to treat the said pathologies.

- 25 The above modified polypeptides may be obtained using combinatory chemistry, in which it is possible to systematically vary portions of the polypeptide before testing them on models, cell cultures or microorganisms for example, so as to select the compounds which are the most active or which exhibit the desired properties.

 Chemical synthesis also has the advantage of being able to use:

- 30 - nonnatural amino acids, or
- nonpeptide bonds.

 Accordingly, in order to extend the life of the polypeptides according to the invention, it may be advantageous to use nonnatural amino acids, for example in the D form, or alternatively amino acid analogues, in particular sulphur-containing forms for example.

- 35 Finally, the structure of the polypeptides according to the invention, its homologous or modified forms, as well as the corresponding fragments may be integrated into chemical structures of the polypeptide type and the like. Accordingly, it may be advantageous to provide at the N- and C-

terminal ends compounds which are not recognized by proteases.

Also forming part of the invention are the nucleotide sequences encoding a polypeptide according to the invention. Described below are ORF nucleotide sequences encoding polypeptides exhibiting particularly preferable characteristics. For each group of preferred ORFS described below, it is to be understood that in addition to the individual ORFs listed, in instances wherein such ORFs are present as part of "combined" ORFs, the "combined" ORFs are also to be included within the preferred group.

More particularly, the subject of the invention is nucleotide sequences, characterized in that they encode a polypeptide of the cellular envelope, preferably of the outer cellular envelope of *Chlamydia pneumoniae* or one of its representative fragments, such as for example the predominant proteins of the outer membrane, the adhesion proteins or the proteins entering into the composition of the Chlamydia wall. Among these sequences, the sequences comprising a nucleotide sequence chosen from the following sequences are most preferred:

ORF15; ORF25; ORF26; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF35;
ORF68; ORF124; ORF275; ORF291; ORF294; ORF327; ORF342; ORF364; ORF374; ORF380;
ORF414; ORF439; ORF466; ORF467; ORF468; ORF469; ORF470; ORF472; ORF474; ORF476;
ORF477; ORF478; ORF479; ORF480; ORF482; ORF485; ORF500; ORF501; ORF503; ORF504;
ORF505; ORF506; ORF520; ORF578; ORF580; ORF581; ORF595; ORF596; ORF597; ORF737;
ORF830; ORF834; ORF836; ORF893; ORF917; ORF932; ORF976; ORF1035; ORF1045; ORF1090
and one of their representative fragments.

The structure of the cytoplasmic membranes and of the wall of bacteria is dependent on the associated proteins. The structure of the cytoplasmic membrane makes it impermeable to water, to water-soluble substances and to small-sized molecules (ions, small inorganic molecules, peptides or proteins). To enter into or to interfere with a cell or a bacterium, a ligand must establish a special relationship with a protein anchored in the cytoplasmic membrane (the receptor). These proteins which are anchored on the membrane play an important role in metabolism since they control the exchanges in the bacterium. These exchanges apply to molecules of interest for the bacterium (small molecules such as sugars and small peptides) as well as undesirable molecules for the bacterium such as antibiotics or heavy metals.

The double lipid layer structure of the membrane requires the proteins which are inserted therein to have hydrophobic domains of about twenty amino acids forming an alpha helix. Predominantly hydrophobic and potentially transmembrane regions may be predicted from the primary sequence of the proteins, itself deduced from the nucleotide sequence. The presence of one or more putative transmembrane domains raises the possibility for a protein to be associated with the cytoplasmic membrane and to be able to play an important metabolic role therein or alternatively for the protein thus exposed to be able to exhibit potentially protective epitopes.

If the proteins inserted into the membrane exhibit several transmembrane domains

capable of interacting with one another via electrostatic bonds, it then becomes possible for these proteins to form pores which go across the membrane which becomes permeable for a number of substances. It should be noted that proteins which do not have transmembrane domains may also be anchored by the intermediacy of fatty acids in the cytoplasmic membrane, it being possible for the
 5 breaking of the bond between the protein and its anchor in some cases to be responsible for the release of the peptide outside the bacterium.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 1 and 3 transmembrane domains and in that they comprise a
 10 nucleotide sequence chosen from the following sequences:

ORF2; ORF3; ORF6; ORF9; ORF10; ORF11; ORF13; ORF14; ORF16; ORF18; ORF19; ORF20;
 ORF21; ORF22; ORF25; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF34;
 ORF35; ORF37; ORF39; ORF41; ORF42; ORF44; ORF45; ORF46; ORF47; ORF48; ORF49;
 ORF50; ORF53; ORF54; ORF56; ORF57; ORF59; ORF60; ORF61; ORF62; ORF63; ORF64;
 15 ORF65; ORF66; ORF69; ORF72; ORF73; ORF74; ORF76; ORF77; ORF78; ORF79; ORF80;
 ORF82; ORF84; ORF85; ORF86; ORF88; ORF89; ORF90; ORF91; ORF92; ORF93; ORF95;
 ORF96; ORF98; ORF99; ORF100; ORF101; ORF102; ORF103; ORF104; ORF105; ORF106;
 ORF107; ORF108; ORF114; ORF117; ORF118; ORF122; ORF123; ORF124; ORF125; ORF129;
 ORF130; ORF131; ORF132; ORF133; ORF134; ORF135; ORF137; ORF138; ORF139; ORF140;
 20 ORF141; ORF142; ORF143; ORF145; ORF146; ORF147; ORF150; ORF151; ORF152; ORF156;
 ORF157; ORF158; ORF159; ORF160; ORF161; ORF162; ORF164; ORF166; ORF167; ORF170;
 ORF173; ORF175; ORF176; ORF178; ORF179; ORF180; ORF182; ORF183; ORF184; ORF185;
 ORF186; ORF187; ORF188; ORF189; ORF190; ORF191; ORF192; ORF194; ORF195; ORF196;
 ORF197; ORF198; ORF199; ORF200; ORF201; ORF202; ORF205; ORF207; ORF208; ORF209;
 25 ORF210; ORF212; ORF215; ORF219; ORF220; ORF224; ORF226; ORF227; ORF228; ORF231;
 ORF232; ORF233; ORF234; ORF235; ORF236; ORF238; ORF239; ORF240; ORF241; ORF242;
 ORF244; ORF247; ORF251; ORF252; ORF253; ORF255; ORF256; ORF257; ORF258; ORF260;
 ORF262; ORF263; ORF266; ORF267; ORF268; ORF269; ORF270; ORF273; ORF274; ORF276;
 ORF278; ORF279; ORF280; ORF281; ORF282; ORF283; ORF284; ORF286; ORF287; ORF289;
 30 ORF290; ORF291; ORF293; ORF294; ORF297; ORF304; ORF305; ORF307; ORF308; ORF309;
 ORF310; ORF311; ORF313; ORF314; ORF315; ORF316; ORF318; ORF319; ORF320; ORF321;
 ORF322; ORF323; ORF324; ORF325; ORF326; ORF331; ORF332; ORF336; ORF338; ORF339;
 ORF341; ORF344; ORF345; ORF346; ORF350; ORF352; ORF353; ORF356; ORF357; ORF358;
 ORF359; ORF360; ORF362; ORF365; ORF366; ORF367; ORF370; ORF372; ORF373; ORF376;
 35 ORF377; ORF378; ORF379; ORF381; ORF382; ORF383; ORF384; ORF385; ORF386; ORF387;
 ORF390; ORF392; ORF393; ORF394; ORF396; ORF398; ORF399; ORF400; ORF404; ORF408;
 ORF410; ORF411; ORF413; ORF416; ORF417; ORF418; ORF420; ORF422; ORF424; ORF427;

ORF428; ORF429; ORF430; ORF431; ORF433; ORF434; ORF437; ORF440; ORF441; ORF442;
ORF443; ORF444; ORF445; ORF447; ORF450; ORF451; ORF452; ORF455; ORF456; ORF459;
ORF460; ORF461; ORF462; ORF463; ORF464; ORF465; ORF467; ORF469; ORF471; ORF474;
ORF475; ORF476; ORF477; ORF479; ORF482; ORF483; ORF484; ORF485; ORF486; ORF487;
5 ORF488; ORF491; ORF493; ORF494; ORF497; ORF498; ORF499; ORF503; ORF508; ORF509;
ORF510; ORF512; ORF514; ORF515; ORF516; ORF517; ORF518; ORF520; ORF521; ORF523;
ORF525; ORF527; ORF528; ORF529; ORF530; ORF531; ORF533; ORF534; ORF535; ORF536;
ORF537; ORF540; ORF541; ORF543; ORF544; ORF545; ORF546; ORF548; ORF549; ORF551;
ORF553; ORF554; ORF555; ORF556; ORF557; ORF558; ORF559; ORF560; ORF562; ORF563;
10 ORF564; ORF565; ORF566; ORF569; ORF571; ORF573; ORF576; ORF577; ORF581; ORF583;
ORF584; ORF585; ORF586; ORF588; ORF591; ORF592; ORF594; ORF595; ORF596; ORF597;
ORF599; ORF600; ORF603; ORF605; ORF608; ORF614; ORF615; ORF620; ORF621; ORF622;
ORF623; ORF624; ORF625; ORF629; ORF630; ORF631; ORF633; ORF634; ORF637; ORF642;
ORF644; ORF645; ORF647; ORF648; ORF652; ORF654; ORF655; ORF657; ORF658; ORF659;
15 ORF660; ORF661; ORF664; ORF665; ORF666; ORF667; ORF670; ORF671; ORF672; ORF673;
ORF674; ORF676; ORF679; ORF681; ORF684; ORF687; ORF688; ORF689; ORF690; ORF693;
ORF694; ORF695; ORF696; ORF697; ORF698; ORF699; ORF700; ORF701; ORF703; ORF705;
ORF706; ORF707; ORF708; ORF710; ORF712; ORF715; ORF716; ORF717; ORF718; ORF719;
ORF721; ORF722; ORF723; ORF725; ORF726; ORF727; ORF728; ORF729; ORF730; ORF731;
20 ORF733; ORF736; ORF737; ORF738; ORF740; ORF741; ORF742; ORF743; ORF747; ORF748;
ORF750; ORF752; ORF754; ORF755; ORF756; ORF757; ORF759; ORF760; ORF761; ORF762;
ORF763; ORF764; ORF765; ORF766; ORF767; ORF768; ORF772; ORF774; ORF775; ORF777;
ORF781; ORF783; ORF788; ORF791; ORF792; ORF793; ORF794; ORF795; ORF796; ORF797;
ORF798; ORF799; ORF802; ORF803; ORF806; ORF807; ORF808; ORF809; ORF810; ORF811;
25 ORF813; ORF814; ORF815; ORF816; ORF817; ORF819; ORF820; ORF821; ORF823; ORF824;
ORF827; ORF829; ORF830; ORF831; ORF833; ORF834; ORF835; ORF837; ORF844; ORF845;
ORF846; ORF847; ORF848; ORF849; ORF850; ORF851; ORF852; ORF854; ORF855; ORF856;
ORF857; ORF859; ORF860; ORF862; ORF865; ORF866; ORF868; ORF869; ORF870; ORF871;
ORF872; ORF874; ORF877; ORF878; ORF879; ORF880; ORF881; ORF882; ORF884; ORF885;
30 ORF888; ORF889; ORF890; ORF891; ORF892; ORF894; ORF895; ORF896; ORF897; ORF899;
ORF900; ORF902; ORF903; ORF904; ORF905; ORF909; ORF910; ORF912; ORF913; ORF914;
ORF915; ORF917; ORF918; ORF919; ORF921; ORF923; ORF924; ORF926; ORF927; ORF928;
ORF929; ORF930; ORF931; ORF937; ORF938; ORF939; ORF941; ORF943; ORF948; ORF951;
ORF952; ORF953; ORF958; ORF960; ORF963; ORF964; ORF965; ORF968; ORF970; ORF974;
35 ORF975; ORF977; ORF979; ORF980; ORF981; ORF983; ORF984; ORF985; ORF987; ORF989;
ORF992; ORF993; ORF997; ORF998; ORF999; ORF1001; ORF1002; ORF1004; ORF1005;
ORF1009; ORF1013; ORF1014; ORF1015; ORF1016; ORF1019; ORF1021; ORF1023; ORF1024;

ORF1029; ORF1031; ORF1033; ORF1034; ORF1039; ORF1041; ORF1042; ORF1045;
 ORF1047; ORF1049; ORF1051; ORF1052; ORF1053; ORF1054; ORF1056; ORF1059; ORF1061;
 ORF1062; ORF1063; ORF1064; ORF1065; ORF1067; ORF1075; ORF1077; ORF1078; ORF1079;
 ORF1080; ORF1081; ORF1089; ORF1095; ORF1097; ORF1098; ORF1099; ORF1101; ORF1102;
 5 ORF1103; ORF1106; ORF1107; ORF1108; ORF1109; ORF1110; ORF1113; ORF1116; ORF1118;
 ORF1119; ORF1121; ORF1123; ORF1124; ORF1126; ORF1128; ORF1130; ORF1131; ORF1133;
 ORF1134; ORF1136; ORF1137 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,
 characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its
 10 representative fragments, having between 4 and 6 transmembrane domains and in that they comprise a
 nucleotide sequence chosen from the following sequences:

ORF5; ORF7; ORF8; ORF15; ORF36; ORF38; ORF51; ORF55; ORF58; ORF67; ORF70; ORF81;
 ORF97; ORF110; ORF111; ORF115; ORF119; ORF126; ORF128; ORF148; ORF155; ORF163;
 ORF165; ORF168; ORF169; ORF171; ORF172; ORF174; ORF177; ORF181; ORF193; ORF203;
 15 ORF213; ORF214; ORF216; ORF217; ORF221; ORF222; ORF225; ORF229; ORF243; ORF246;
 ORF248; ORF254; ORF261; ORF285; ORF288; ORF292; ORF296; ORF298; ORF299; ORF301;
 ORF303; ORF317; ORF328; ORF329; ORF351; ORF354; ORF355; ORF364; ORF371; ORF374;
 ORF375; ORF391; ORF395; ORF401; ORF403; ORF405; ORF409; ORF414; ORF419; ORF421;
 ORF423; ORF425; ORF438; ORF448; ORF453; ORF458; ORF466; ORF468; ORF470; ORF480;
 20 ORF489; ORF490; ORF496; ORF501; ORF504; ORF505; ORF506; ORF511; ORF513; ORF519;
 ORF526; ORF532; ORF538; ORF539; ORF547; ORF550; ORF561; ORF568; ORF570; ORF574;
 ORF578; ORF579; ORF580; ORF582; ORF589; ORF593; ORF598; ORF601; ORF604; ORF610;
 ORF613; ORF617; ORF626; ORF632; ORF635; ORF638; ORF640; ORF641; ORF646; ORF649;
 ORF650; ORF651; ORF686; ORF711; ORF724; ORF732; ORF734; ORF744; ORF745; ORF749;
 25 ORF751; ORF769; ORF770; ORF771; ORF773; ORF776; ORF779; ORF780; ORF785; ORF787;
 ORF789; ORF801; ORF805; ORF812; ORF822; ORF825; ORF826; ORF839; ORF841; ORF843;
 ORF853; ORF861; ORF875; ORF876; ORF886; ORF893; ORF898; ORF906; ORF907; ORF908;
 ORF920; ORF922; ORF925; ORF933; ORF935; ORF936; ORF944; ORF946; ORF947; ORF954;
 ORF959; ORF961; ORF966; ORF967; ORF972; ORF978; ORF995; ORF996; ORF1000; ORF1003;
 30 ORF1010; ORF1011; ORF1012; ORF1017; ORF1020; ORF1030; ORF1036; ORF1038; ORF1043;
 ORF1046; ORF1048; ORF1050; ORF1058; ORF1071; ORF1073; ORF1084; ORF1085; ORF1086;
 ORF1087; ORF1091; ORF1092; ORF1094; ORF1096; ORF1100; ORF1104; ORF1111; ORF1112;
 ORF1114; ORF1117; ORF1122; ORF1125 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the
 35 invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or
 one of its representative fragments, having at least 7 transmembrane domains and in that they
 comprise a nucleotide sequence chosen from the following sequences:

ORF17; ORF52; ORF68; ORF83; ORF87; ORF109; ORF112; ORF113; ORF120; ORF121;
 ORF127; ORF153; ORF204; ORF211; ORF218; ORF223; ORF275; ORF277; ORF295; ORF300;
 ORF302; ORF306; ORF327; ORF335; ORF342; ORF343; ORF347; ORF349; ORF361; ORF363;
 ORF369; ORF380; ORF388; ORF389; ORF397; ORF415; ORF432; ORF439; ORF446; ORF449;
 5 ORF472; ORF478; ORF500; ORF522; ORF524; ORF567; ORF575; ORF602; ORF606; ORF609;
 ORF636; ORF639; ORF643; ORF653; ORF668; ORF692; ORF702; ORF704; ORF713; ORF720;
 ORF778; ORF784; ORF800; ORF836; ORF838; ORF842; ORF864; ORF867; ORF883; ORF901;
 ORF916; ORF932; ORF934; ORF940; ORF942; ORF950; ORF956; ORF971; ORF973; ORF976;
 ORF988; ORF994; ORF1018; ORF1028; ORF1035; ORF1037; ORF1044; ORF1055; ORF1057;
 10 ORF1068; ORF1069; ORF1070; ORF1072; ORF1082; ORF1088; ORF1105; ORF1132; ORF1135
 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,
 characterized in that they encode a *Chlamydia pneumoniae* surface exposed polypeptide (e.g., an outer
 membrane protein) or one of its representative fragments, said nucleotide sequences comprising a
 15 nucleotide sequence chosen from the following sequences:

ORF 15, ORF 25, ORF 26, ORF 27, ORF 28, ORF 29, ORF 30, ORF 31, ORF 32, ORF 33, ORF 35,
 ORF 36, ORF 1257, ORF 280, ORF 291, ORF 314, ORF 354, ORF 380, ORF 1266, ORF 466, ORF
 467, ORF 468, ORF 469, ORF 470, ORF 472, ORF 474, ORF 476, ORF 477, ORF 478, ORF 479,
 ORF 480, ORF 482, ORF 483, ORF 485, ORF 486, ORF 500, ORF 501, ORF 503, ORF 504, ORF
 20 505, ORF 506, ORF 507, ORF 1268, ORF 1269, ORF 543, ORF 544, ORF 578, ORF 579, ORF 580,
 ORF 581, ORF 595, ORF 596, ORF 597, ORF 1271, ORF 633, ORF 637, ORF 699, ORF 706, ORF
 737, ORF 744, ORF 1273, ORF 751, ORF 775, ORF 776, ORF 777, ORF 793, ORF 815, ORF 830,
 ORF 1221, ORF 849, ORF 851, ORF 852, ORF 874, ORF 891, ORF 922, ORF 940, ORF 1231, ORF
 1281, ORF 1035, ORF 1079, ORF 1087, ORF 1108, and one of their representative fragments.

25 Preferably, the invention relates to the nucleotide sequences according to the invention,
 characterized in that they encode a *Chlamydia pneumoniae* lipoprotein or one of its representative
 fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following
 sequences:

ORF 3, ORF 10, ORF 11, ORF 16, ORF 1254, ORF 1255, ORF 38, ORF 1256, ORF 62, ORF 85,
 30 ORF 1258, ORF 115, ORF 1151, ORF 151, ORF 1259, ORF 173, ORF 1261, ORF 186, ORF 194,
 ORF 205, ORF 214, ORF 216, ORF 217, ORF 238, ORF 1177, ORF 280, ORF 291, ORF 317, ORF
 327, ORF 354, ORF 364, ORF 367, ORF 414, ORF 432, ORF 1192, ORF 460, ORF 1267, ORF 1268,
 ORF 520, ORF 536, ORF 1270, ORF 576, ORF 597, ORF 603, ORF 609, ORF 637, ORF 1272, ORF
 652, ORF 1213, ORF 699, ORF 705, ORF 706, ORF 708, ORF 711, ORF 727, ORF 1274, ORF 800,
 35 ORF 814, ORF 825, ORF 829, ORF 830, ORF 831, ORF 844, ORF 849, ORF 1275, ORF 1276, ORF
 1277, ORF 872, ORF 878, ORF 880, ORF 891, ORF 892, ORF 1278, ORF 1279, ORF 1280, ORF
 941, ORF 942, ORF 1282, ORF 1283, ORF 952, ORF 988, ORF 998, ORF 1009, ORF 1285, ORF

1235, ORF 1028, ORF 1056, ORF 1070, ORF 1287, ORF 1087, ORF 1288, ORF 1289, ORF 1098, ORF 1246, ORF 1291, ORF 1108, ORF 1109, ORF 1112, ORF 1133, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,
5 characterized in that they encode a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 316, ORF 564, ORF 610, ORF 647, ORF 1211, ORF 688, ORF 924, and one of their representative fragments.

Preferably the invention relates to additional LPS-related nucleotide sequences according
10 to the invention, characterized in that they encode:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octulosonic acid)-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 177, ORF 1156, ORF 245, ORF 767, and one of their representative fragments;

15 (b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 74, and one of its representative fragments;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the
20 following sequences: ORF 1286, ORF 1039, and one of their representative fragments; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 689, ORF 690, ORF 691, ORF 1037, and one of their representative fragments.

25 Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide containing RGD (Arg-Gly-Asp) attachment sites or one of its representative fragments.

(a) RGD-containing proteins that are outer membrane proteins, are more likely to play a
30 role in cell attachment. ORFs that encoded a protein containing an RGD sequence and also were classified as outer membrane proteins are ORF 468 and its representative fragments.

(b) An RGD-encoding ORF that showed homology to *cds1*, *cds2*, and *copN* type III
35 virulence loci in *Chlamydia psittaci* (Hsia, R. et al. (1997), Type III secretion genes identify a putative virulence locus of *Chlamydia*. Molecular Microbiology 25:351-359) is ORF 350, and its representative fragments.

- 5 (c) The outer membrane of *Chlamydia* is made of cysteine-rich proteins that form a network of both intra and inter molecular disulfide links. This contributes to the integrity of the membrane since *Chlamydia* lacks the peptidoglycan layer that other gram-negative bacteria have. Cysteine-rich proteins that have the RGD sequence are also considered to be potential vaccine candidates. Cysteine-rich proteins were defined as proteins that had more than 3.0% cysteine in their primary amino acid sequence, above the mean genomic ORF cysteine content. The corresponding ORFs are: ORF 1290, ORF 1294, ORF 1296, and one of their representative fragments.
- 10 (d) The outer membrane of *Chlamydia* may also contain small proteins that have cysteines in their N- and C-terminus that may contribute to the network formed by disulfide linkages. These proteins may be anchored in the outer membrane via their N-terminus and may have their C-terminus exposed, which then can interact with the host cells. Alternatively, these proteins may be anchored in the outer membrane via both N-and C-terminus and may have regions in the middle that may be exposed which can in turn interact with the host cells. ORFs encoding polypeptides that contain cysteines in their first 30 amino acids and also contain an RGD sequence are: ORF 105, ORF 106, ORF 114, ORF 170, ORF 171, ORF 1264, ORF 268, ORF 1265, ORF 350, ORF 393, ORF 394, ORF 451, ORF 452, ORF 453, ORF 473, ORF 499, ORF 515, ORF 519, ORF 525, ORF 526, ORF 538, ORF 611, ORF 645, ORF 686, ORF 700, ORF 746, ORF 755, ORF 756, ORF 757, ORF 789, ORF 814, ORF 855, ORF 856, ORF 878, ORF 957, ORF 958, ORF 989, ORF 1290, and one of their representative fragments.
- 25 (e) RGD-containing ORFs homologous to RGD-containing ORFs from *Chlamydia trachomatis* are:
ORF 114, ORF 468, ORF 755, ORF 756, ORF 757, ORF 855, ORF 856, ORF 905, ORF 913, ORF 914, ORF 915, and one of their representative fragments.
- 30 Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* Type III or other, non-type III secreted polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences:
- 35 ORF 25, ORF 28, ORF 29, ORF 33, ORF 308, ORF 309, ORF 343, ORF 344, ORF 345, ORF 367, ORF 414, ORF 415, ORF 480, ORF 550, ORF 579, ORF 580, ORF 581, ORF 597, ORF 699, ORF 744, ORF 751, ORF 776, ORF 866, ORF 874, ORF 883, ORF 884, ORF 888, ORF 891, ORF 1293,

and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence
5 chosen from the following sequences: ORF 267, ORF 271, ORF 419, ORF 590, ORF 932, ORF 1292, ORF 1295, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode *Chlamydia pneumoniae* polypeptides not found in *Chlamydia trachomatis* (Blastp. $P > e^{-10}$), said nucleotide sequences comprising a nucleotide sequence chosen from
10 the following sequences: ORF 7, ORF 8, ORF 9, ORF 16, ORF 17, ORF 18, ORF 19, ORF 20, ORF 21, ORF 22, ORF 1254, ORF 23, ORF 1255, ORF 24, ORF 1139, ORF 1140, ORF 46, ORF 47, ORF 51, ORF 60, ORF 1256, ORF 61, ORF 62, ORF 63, ORF 64, ORF 1257, ORF 65, ORF 66, ORF 67, ORF 68, ORF 1143, ORF 1145, ORF 83, ORF 84, ORF 1146, ORF 85, ORF 86, ORF 87, ORF 1258, ORF 116, ORF 117, ORF 125, ORF 1148, ORF 143, ORF 1150, ORF 1151, ORF 144, ORF 145, ORF
15 147, ORF 148, ORF 149, ORF 150, ORF 152, ORF 1259, ORF 162, ORF 166, ORF 1154, ORF 167, ORF 1261, ORF 1156, ORF 1157, ORF 178, ORF 179, ORF 1158, ORF 182, ORF 183, ORF 184, ORF 185, ORF 1159, ORF 186, ORF 1160, ORF 187, ORF 188, ORF 189, ORF 190, ORF 1161, ORF 1162, ORF 191, ORF 192, ORF 194, ORF 195, ORF 1163, ORF 196, ORF 201, ORF 202, ORF 209, ORF 212, ORF 221, ORF 224, ORF 1167, ORF 226, ORF 227, ORF 228, ORF 229, ORF 230, ORF
20 231, ORF 232, ORF 1169, ORF 1170, ORF 1171, ORF 234, ORF 235, ORF 236, ORF 1172, ORF 243, ORF 251, ORF 252, ORF 1176, ORF 253, ORF 255, ORF 254, ORF 256, ORF 1177, ORF 1178, ORF 262, ORF 263, ORF 1264, ORF 278, ORF 279, ORF 1180, ORF 280, ORF 290, ORF 291, ORF 292, ORF 296, ORF 1181, ORF 297, ORF 298, ORF 300, ORF 1265, ORF 322, ORF 324, ORF 325, ORF 370, ORF 1186, ORF 371, ORF 372, ORF 1187, ORF 373, ORF 378, ORF 1266, ORF 382, ORF
25 383, ORF 384, ORF 385, ORF 386, ORF 1188, ORF 1189, ORF 391, ORF 392, ORF 398, ORF 400, ORF 403, ORF 1191, ORF 423, ORF 435, ORF 445, ORF 450, ORF 1193, ORF 456, ORF 460, ORF 461, ORF 465, ORF 1196, ORF 471, ORF 473, ORF 475, ORF 481, ORF 484, ORF 487, ORF 488, ORF 489, ORF 490, ORF 491, ORF 492, ORF 493, ORF 494, ORF 495, ORF 496, ORF 497, ORF 498, ORF 499, ORF 502, ORF 1267, ORF 1268, ORF 508, ORF 510, ORF 509, ORF 512, ORF 515,
30 ORF 519, ORF 1197, ORF 521, ORF 1198, ORF 522, ORF 524, ORF 528, ORF 534, ORF 537, ORF 1269, ORF 1270, ORF 548, ORF 551, ORF 557, ORF 1201, ORF 1203, ORF 562, ORF 566, ORF 593, ORF 595, ORF 600, ORF 1271, ORF 604, ORF 611, ORF 612, ORF 614, ORF 616, ORF 625, ORF 627, ORF 628, ORF 629, ORF 631, ORF 641, ORF 1272, ORF 648, ORF 1212, ORF 663, ORF 685, ORF 707, ORF 714, ORF 715, ORF 716, ORF 717, ORF 722, ORF 746, ORF 1273, ORF 761,
35 ORF 764, ORF 770, ORF 1217, ORF 783, ORF 1274, ORF 803, ORF 815, ORF 1220, ORF 835, ORF 1221, ORF 844, ORF 845, ORF 846, ORF 847, ORF 848, ORF 849, ORF 850, ORF 851, ORF 1275, ORF 852, ORF 862, ORF 1276, ORF 1277, ORF 873, ORF 1223, ORF 892, ORF 919, ORF 1225,

ORF 1278, ORF 926, ORF 1228, ORF 1229, ORF 1230, ORF 1279, ORF 1281, ORF 1282, ORF 1283, ORF 948, ORF 950, ORF 949, ORF 951, ORF 980, ORF 982, ORF 1233, ORF 999, ORF 1000, ORF 1001, ORF 1002, ORF 1008, ORF 1285, ORF 1235, ORF 1016, ORF 1019, ORF 1027, ORF 1036, ORF 1241, ORF 1048, ORF 1049, ORF 1050, ORF 1053, ORF 1054, ORF 1064, ORF 1076, ORF 1091, ORF 1288, ORF 1093, ORF 1289, ORF 1101, ORF 1103, ORF 1245, ORF 1246, ORF 1247, ORF 1290, ORF 1291, ORF 1115, ORF 1116, ORF 1118, ORF 1120, ORF 1249, ORF 1121, ORF 1250, ORF 1126, ORF 1251, ORF 1127, ORF 1128, ORF 1130, ORF 1129, ORF 1131, ORF 1136, ORF 1253, ORF 1292, ORF 1294, ORF 1295, ORF 1296, and one of their representative fragments.

10 Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, such as for example triose phosphate isomerase or pyruvate kinase, and in that they comprise a nucleotide sequence chosen from the following sequences:

15 ORF2; ORF55; ORF56; ORF69; ORF75; ORF80; ORF100; ORF110; ORF114; ORF120; ORF121; ORF157; ORF160; ORF161; ORF172; ORF180; ORF181; ORF198; ORF200; ORF225; ORF248; ORF249; ORF276; ORF277; ORF318; ORF319; ORF320; ORF323; ORF331; ORF347; ORF375; ORF376; ORF381; ORF393; ORF394; ORF395; ORF396; ORF409; ORF446; ORF447; ORF448; ORF449; ORF513; ORF516; ORF571; ORF647; ORF662; ORF697; ORF718; ORF793; ORF794; 20 ORF808; ORF809; ORF838; ORF839; ORF840; ORF853; ORF854; ORF918; ORF923; ORF929; ORF931; ORF938; ORF939; ORF958; ORF959; ORF960; ORF966; ORF995; ORF1021; ORF1040; ORF1041; ORF1042; ORF1085; ORF1100; ORF1102; ORF1117; ORF1118; ORF1119; ORF1120; ORF1135 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the 25 invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, such as for example CTP synthetase or GMP synthetase, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF77; ORF78; ORF138; ORF189; ORF190; ORF233; ORF246; ORF338; ORF412; ORF421; 30 ORF438; ORF607; ORF648; ORF657; ORF740; ORF783; ORF967; ORF989; ORF990; ORF992; ORF1011; ORF1058; ORF1059; ORF1073; ORF1074 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, such as for example 35 DNA polymerases or DNA topoisomerases, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF14; ORF59; ORF70; ORF71; ORF97; ORF113; ORF137; ORF141; ORF169; ORF285; ORF287;

ORF288; ORF313; ORF326; ORF358; ORF411; ORF443; ORF548; ORF569; ORF601; ORF651;
ORF654; ORF658; ORF659; ORF664; ORF665; ORF694; ORF698; ORF704; ORF760; ORF762;
ORF763; ORF786; ORF787; ORF788; ORF801; ORF802; ORF812; ORF819; ORF822; ORF870;
ORF897; ORF898; ORF902; ORF908; ORF916; ORF954; ORF955; ORF961; ORF983; ORF996;
5 ORF1007; ORF1012; ORF1013; ORF1014; ORF1015; ORF1038; ORF1137 and one of their
representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its
representative fragments which is involved in the metabolism of amino acids or polypeptides, such as
10 for example serine hydroxymethyl transferase or the proteins which load amino acids onto transfer
RNAs, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF99; ORF111; ORF127; ORF134; ORF140; ORF174; ORF175; ORF176; ORF353; ORF377;
ORF404; ORF523; ORF539; ORF559; ORF561; ORF586; ORF598; ORF609; ORF636; ORF687;
ORF700; ORF701; ORF759; ORF790; ORF857; ORF861; ORF904; ORF936; ORF952; ORF962;
15 ORF963; ORF964; ORF965; ORF991; ORF1003; ORF1004; ORF1005; ORF1018; ORF1067;
ORF1110; ORF1111; ORF1112; ORF1114; ORF1121; ORF1122; ORF1123; ORF1124; ORF1125
and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its
20 representative fragments which is involved in the metabolism of polypeptides, such as for example
protein kinases or proteases, and in that they comprise a nucleotide sequence chosen from the
following sequences:

ORF4; ORF44; ORF45; ORF48; ORF54; ORF112; ORF130; ORF155; ORF163; ORF212; ORF257;
ORF307; ORF343; ORF405; ORF416; ORF458; ORF540; ORF541; ORF542; ORF543; ORF544;
25 ORF560; ORF594; ORF652; ORF699; ORF723; ORF747; ORF817; ORF827; ORF871; ORF909;
ORF910; ORF911; ORF912; ORF1023; ORF1051; ORF1052; ORF1081 and one of their
representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its
30 representative fragments which is involved in the metabolism of fatty acids, such as for example
succinyl-CoA-synthesizing proteins or phosphatidylserine synthetase, and in that they comprise a
nucleotide sequence chosen from the following sequences:

ORF76; ORF284; ORF308; ORF309; ORF310; ORF311; ORF312; ORF425; ORF433; ORF565;
ORF688; ORF690; ORF691; ORF767; ORF797; ORF894; ORF895; ORF994; ORF1020; ORF1030;
35 ORF1033; ORF1034; ORF1046; ORF1047; ORF1057 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its

representative fragments which is involved in the synthesis of the wall, such as for example KDO transferase, and the proteins responsible for the attachment of certain sugars onto the exposed proteins, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF49; ORF50; ORF177; ORF178; ORF245; ORF610; ORF972; ORF974; ORF978; ORF1037 and

5 one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, such as for example initiation factors, RNA polymerases or certain chaperone proteins, and in that

10 they comprise a nucleotide sequence chosen from the following sequences:

ORF90; ORF92; ORF131; ORF151; ORF199; ORF333; ORF334; ORF336; ORF379; ORF589; ORF590; ORF619; ORF630; ORF649; ORF739; ORF741; ORF806; ORF821; ORF843; ORF968; ORF971; ORF1061 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative fragments, such as for example the ribosomal proteins L21, L27 and S10, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF93; ORF94; ORF95; ORF136; ORF259; ORF332; ORF348; ORF583; ORF584; ORF588; ORF591; ORF592; ORF663; ORF666; ORF667; ORF669; ORF670; ORF671; ORF672; ORF673; 20 ORF674; ORF675; ORF676; ORF677; ORF678; ORF679; ORF680; ORF681; ORF683; ORF684; ORF738; ORF781; ORF1008; ORF1024; ORF1025; ORF1066 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transport polypeptide or one of its representative fragments, such as for example the proteins for transporting amino acids, sugars and certain oligopeptides, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF40; ORF41; ORF52; ORF105; ORF106; ORF107; ORF109; ORF133; ORF210; ORF211; ORF214; ORF215; ORF216; ORF217; ORF218; ORF219; ORF220; ORF223; ORF242; ORF260; 30 ORF293; ORF299; ORF366; ORF369; ORF575; ORF602; ORF638; ORF639; ORF640; ORF643; ORF653; ORF702; ORF703; ORF724; ORF732; ORF855; ORF856; ORF901; ORF906; ORF933; ORF942; ORF1043; ORF1086; ORF1105 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the virulence process, such as for example the proteins analogous to the *Escherichia coli* vacB protein, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF546; ORF550; ORF778; ORF779; ORF886 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, such as
5 for example proteins homologous to proteins in the secretory system of certain bacteria such as the *Salmonellae* or the *Yersiniae*, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF751; ORF874; ORF875; ORF876; ORF883; ORF884; ORF885 and one of their representative fragments.

10 Preferably, the invention also relates to a nucleotide sequence according to the invention, characterized in that they encode a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments (with a Blast E value of $>10^{-5}$), and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF7; ORF8; ORF17; ORF18; ORF19; ORF20; ORF22; ORF23; ORF24; ORF51; ORF60; ORF63;
15 ORF65; ORF66; ORF67; ORF83; ORF84; ORF86; ORF87; ORF125; ORF143; ORF144; ORF179;
ORF182; ORF184; ORF185; ORF187; ORF221; ORF252; ORF254; ORF278; ORF279; ORF387;
ORF388; ORF397; ORF1048; ORF1049; ORF1050; ORF1128; ORF1130; ORF1131 and one of their representative fragments.

Also forming part of the invention are polypeptides encoded by the polynucleotides of
20 the invention, as well as fusion polypeptides comprising such polypeptides. In one embodiment, the polypeptides and fusion polypeptides immunoreact with seropositive serum of an individual infected with *Chlamydia pneumoniae*. For example, described below, are polypeptide sequences exhibiting particularly preferable characteristics. For each group of preferred polypeptides described below, it is to be understood that in addition to the individual polypeptides listed, in instances wherein such
25 polypeptides are encoded as part of "combined" ORFs, such "combined" polypeptides are also to be included within the preferred group.

The subject of the invention is also a polypeptide according to the invention, characterized in that it is a polypeptide of the cellular envelope, preferably of the outer cellular envelope, of *Chlamydia pneumoniae* or one of its representative fragments. According to the
30 invention, the said polypeptide is preferably chosen from the polypeptides having the following sequences:

SEQ ID No. 15; SEQ ID No. 25; SEQ ID No. 26; SEQ ID No. 27; SEQ ID No. 28; SEQ ID No. 29;
SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 35; SEQ ID No. 68;
SEQ ID No. 124; SEQ ID No. 275; SEQ ID No. 291; SEQ ID No. 294; SEQ ID No. 327; SEQ ID
35 No. 342; SEQ ID No. 364; SEQ ID No. 374; SEQ ID No. 380; SEQ ID No. 414; SEQ ID No. 439;
SEQ ID No. 466; SEQ ID No. 467; SEQ ID No. 468; SEQ ID No. 469; SEQ ID No. 470; SEQ ID
No. 472; SEQ ID No. 474; SEQ ID No. 476; SEQ ID No. 477; SEQ ID No. 478; SEQ ID No. 479;

SEQ ID No. 480; SEQ ID No. 482; SEQ ID No. 485; SEQ ID No. 500; SEQ ID No. 501;
 SEQ ID No. 503; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 520; SEQ ID
 No. 578; SEQ ID No. 580; SEQ ID No. 581; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597;
 SEQ ID No. 737; SEQ ID No. 830; SEQ ID No. 834; SEQ ID No. 836; SEQ ID No. 893; SEQ ID
 5 No. 917; SEQ ID No. 932; SEQ ID No. 976; SEQ ID No. 1035; SEQ ID No. 1045; SEQ ID No. 1090
 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,
 characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its
 representative fragments, having between 1 and 3 transmembrane domains, and in that it is chosen
 10 from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 3; SEQ ID No. 6; SEQ ID No. 9; SEQ ID No. 10; SEQ ID No. 11;
 SEQ ID No. 13; SEQ ID No. 14; SEQ ID No. 16; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20;
 SEQ ID No. 21; SEQ ID No. 22; SEQ ID No. 25; SEQ ID No. 27; SEQ ID No. 28; SEQ ID
 No. 29; SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 34;
 15 SEQ ID No. 35; SEQ ID No. 37; SEQ ID No. 39; SEQ ID No. 41; SEQ ID No. 42; SEQ ID
 No. 44; SEQ ID No. 45; SEQ ID No. 46; SEQ ID No. 47; SEQ ID No. 48; SEQ ID No. 49;
 SEQ ID No. 50; SEQ ID No. 53; SEQ ID No. 54; SEQ ID No. 56; SEQ ID No. 57; SEQ ID
 No. 59; SEQ ID No. 60; SEQ ID No. 61; SEQ ID No. 62; SEQ ID No. 63; SEQ ID No. 64;
 SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 69; SEQ ID No. 72; SEQ ID No. 73; SEQ ID
 20 No. 74; SEQ ID No. 76; SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 79; SEQ ID No. 80;
 SEQ ID No. 82; SEQ ID No. 84; SEQ ID No. 85; SEQ ID No. 86; SEQ ID No. 88; SEQ ID
 No. 89; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 92; SEQ ID No. 93; SEQ ID No. 95;
 SEQ ID No. 96; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 100; SEQ ID No. 101; SEQ ID
 No. 102; SEQ ID No. 103; SEQ ID No. 104; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107;
 25 SEQ ID No. 108; SEQ ID No. 114; SEQ ID No. 117; SEQ ID No. 118; SEQ ID No. 122; SEQ ID
 No. 123; SEQ ID No. 124; SEQ ID No. 125; SEQ ID No. 129; SEQ ID No. 130; SEQ ID No. 131;
 SEQ ID No. 132; SEQ ID No. 133; SEQ ID No. 134; SEQ ID No. 135; SEQ ID No. 137; SEQ ID
 No. 138; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 141; SEQ ID No. 142; SEQ ID No. 143;
 SEQ ID No. 145; SEQ ID No. 146; SEQ ID No. 147; SEQ ID No. 150; SEQ ID No. 151; SEQ ID
 30 No. 152; SEQ ID No. 156; SEQ ID No. 157; SEQ ID No. 158; SEQ ID No. 159; SEQ ID No. 160;
 SEQ ID No. 161; SEQ ID No. 162; SEQ ID No. 164; SEQ ID No. 166; SEQ ID No. 167; SEQ ID
 No. 170; SEQ ID No. 173; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179;
 SEQ ID No. 180; SEQ ID No. 182; SEQ ID No. 183; SEQ ID No. 184; SEQ ID No. 185; SEQ ID
 No. 186; SEQ ID No. 187; SEQ ID No. 188; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 191;
 35 SEQ ID No. 192; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 196; SEQ ID No. 197; SEQ ID
 No. 198; SEQ ID No. 199; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 202; SEQ ID No. 205;
 SEQ ID No. 207; SEQ ID No. 208; SEQ ID No. 209; SEQ ID No. 210; SEQ ID No. 212; SEQ ID

No. 215; SEQ ID No. 219; SEQ ID No. 220; SEQ ID No. 224; SEQ ID No. 226; SEQ ID No. 227; SEQ ID No. 228; SEQ ID No. 231; SEQ ID No. 232; SEQ ID No. 233; SEQ ID No. 234; SEQ ID No. 235; SEQ ID No. 236; SEQ ID No. 238; SEQ ID No. 239; SEQ ID No. 240; SEQ ID No. 241; SEQ ID No. 242; SEQ ID No. 244; SEQ ID No. 247; SEQ ID No. 251; SEQ ID No. 252;
5 SEQ ID No. 253; SEQ ID No. 255; SEQ ID No. 256; SEQ ID No. 257; SEQ ID No. 258; SEQ ID No. 260; SEQ ID No. 262; SEQ ID No. 263; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 268; SEQ ID No. 269; SEQ ID No. 270; SEQ ID No. 273; SEQ ID No. 274; SEQ ID No. 276; SEQ ID No. 278; SEQ ID No. 279; SEQ ID No. 280; SEQ ID No. 281; SEQ ID No. 282; SEQ ID No. 283; SEQ ID No. 284; SEQ ID No. 286; SEQ ID No. 287; SEQ ID No. 289; SEQ ID No. 290; SEQ ID
10 No. 291; SEQ ID No. 293; SEQ ID No. 294; SEQ ID No. 297; SEQ ID No. 304; SEQ ID No. 305; SEQ ID No. 307; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID No. 311; SEQ ID No. 313; SEQ ID No. 314; SEQ ID No. 315; SEQ ID No. 316; SEQ ID No. 318; SEQ ID No. 319; SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 322; SEQ ID No. 323; SEQ ID No. 324; SEQ ID No. 325; SEQ ID No. 326; SEQ ID No. 331; SEQ ID No. 332; SEQ ID No. 336; SEQ ID No. 338;
15 SEQ ID No. 339; SEQ ID No. 341; SEQ ID No. 344; SEQ ID No. 345; SEQ ID No. 346; SEQ ID No. 350; SEQ ID No. 352; SEQ ID No. 353; SEQ ID No. 356; SEQ ID No. 357; SEQ ID No. 358; SEQ ID No. 359; SEQ ID No. 360; SEQ ID No. 362; SEQ ID No. 365; SEQ ID No. 366; SEQ ID No. 367; SEQ ID No. 370; SEQ ID No. 372; SEQ ID No. 373; SEQ ID No. 376; SEQ ID No. 377; SEQ ID No. 378; SEQ ID No. 379; SEQ ID No. 381; SEQ ID No. 382; SEQ ID No. 383; SEQ ID
20 No. 384; SEQ ID No. 385; SEQ ID No. 386; SEQ ID No. 387; SEQ ID No. 390; SEQ ID No. 392; SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 396; SEQ ID No. 398; SEQ ID No. 399; SEQ ID No. 400; SEQ ID No. 404; SEQ ID No. 408; SEQ ID No. 410; SEQ ID No. 411; SEQ ID No. 413; SEQ ID No. 416; SEQ ID No. 417; SEQ ID No. 418; SEQ ID No. 420; SEQ ID No. 422; SEQ ID No. 424; SEQ ID No. 427; SEQ ID No. 428; SEQ ID No. 429; SEQ ID No. 430; SEQ ID No. 431;
25 SEQ ID No. 433; SEQ ID No. 434; SEQ ID No. 437; SEQ ID No. 440; SEQ ID No. 441; SEQ ID No. 442; SEQ ID No. 443; SEQ ID No. 444; SEQ ID No. 445; SEQ ID No. 447; SEQ ID No. 450; SEQ ID No. 451; SEQ ID No. 452; SEQ ID No. 455; SEQ ID No. 456; SEQ ID No. 459; SEQ ID No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 464; SEQ ID No. 465; SEQ ID No. 467; SEQ ID No. 469; SEQ ID No. 471; SEQ ID No. 474; SEQ ID No. 475; SEQ ID
30 No. 476; SEQ ID No. 477; SEQ ID No. 479; SEQ ID No. 482; SEQ ID No. 483; SEQ ID No. 484; SEQ ID No. 485; SEQ ID No. 486; SEQ ID No. 487; SEQ ID No. 488; SEQ ID No. 491; SEQ ID No. 493; SEQ ID No. 494; SEQ ID No. 497; SEQ ID No. 498; SEQ ID No. 499; SEQ ID No. 503; SEQ ID No. 508; SEQ ID No. 509; SEQ ID No. 510; SEQ ID No. 512; SEQ ID No. 514; SEQ ID No. 515; SEQ ID No. 516; SEQ ID No. 517; SEQ ID No. 518; SEQ ID No. 520; SEQ ID No. 521;
35 SEQ ID No. 523; SEQ ID No. 525; SEQ ID No. 527; SEQ ID No. 528; SEQ ID No. 529; SEQ ID No. 530; SEQ ID No. 531; SEQ ID No. 533; SEQ ID No. 534; SEQ ID No. 535; SEQ ID No. 536; SEQ ID No. 537; SEQ ID No. 540; SEQ ID No. 541; SEQ ID No. 543; SEQ ID No. 544; SEQ ID

No. 545; SEQ ID No. 546; SEQ ID No. 548; SEQ ID No. 549; SEQ ID No. 551; SEQ ID No. 553; SEQ ID No. 554; SEQ ID No. 555; SEQ ID No. 556; SEQ ID No. 557; SEQ ID No. 558; SEQ ID No. 559; SEQ ID No. 560; SEQ ID No. 562; SEQ ID No. 563; SEQ ID No. 564; SEQ ID No. 565; SEQ ID No. 566; SEQ ID No. 569; SEQ ID No. 571; SEQ ID No. 573; SEQ ID No. 576;
5 SEQ ID No. 577; SEQ ID No. 581; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 585; SEQ ID No. 586; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 594; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597; SEQ ID No. 599; SEQ ID No. 600; SEQ ID No. 603; SEQ ID No. 605; SEQ ID No. 608; SEQ ID No. 614; SEQ ID No. 615; SEQ ID No. 620; SEQ ID No. 621; SEQ ID No. 622; SEQ ID No. 623; SEQ ID No. 624; SEQ ID No. 625; SEQ ID No. 629; SEQ ID
10 No. 630; SEQ ID No. 631; SEQ ID No. 633; SEQ ID No. 634; SEQ ID No. 637; SEQ ID No. 642; SEQ ID No. 644; SEQ ID No. 645; SEQ ID No. 647; SEQ ID No. 648; SEQ ID No. 652; SEQ ID No. 654; SEQ ID No. 655; SEQ ID No. 657; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 660; SEQ ID No. 661; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 676;
15 SEQ ID No. 679; SEQ ID No. 681; SEQ ID No. 684; SEQ ID No. 687; SEQ ID No. 688; SEQ ID No. 689; SEQ ID No. 690; SEQ ID No. 693; SEQ ID No. 694; SEQ ID No. 695; SEQ ID No. 696; SEQ ID No. 697; SEQ ID No. 698; SEQ ID No. 699; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 703; SEQ ID No. 705; SEQ ID No. 706; SEQ ID No. 707; SEQ ID No. 708; SEQ ID No. 710; SEQ ID No. 712; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 717; SEQ ID No. 718; SEQ ID
20 No. 719; SEQ ID No. 721; SEQ ID No. 722; SEQ ID No. 723; SEQ ID No. 725; SEQ ID No. 726; SEQ ID No. 727; SEQ ID No. 728; SEQ ID No. 729; SEQ ID No. 730; SEQ ID No. 731; SEQ ID No. 733; SEQ ID No. 736; SEQ ID No. 737; SEQ ID No. 738; SEQ ID No. 740; SEQ ID No. 741; SEQ ID No. 742; SEQ ID No. 743; SEQ ID No. 747; SEQ ID No. 748; SEQ ID No. 750; SEQ ID No. 752; SEQ ID No. 754; SEQ ID No. 755; SEQ ID No. 756; SEQ ID No. 757; SEQ ID No. 759;
25 SEQ ID No. 760; SEQ ID No. 761; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 764; SEQ ID No. 765; SEQ ID No. 766; SEQ ID No. 767; SEQ ID No. 768; SEQ ID No. 772; SEQ ID No. 774; SEQ ID No. 775; SEQ ID No. 777; SEQ ID No. 781; SEQ ID No. 783; SEQ ID No. 788; SEQ ID No. 791; SEQ ID No. 792; SEQ ID No. 793; SEQ ID No. 794; SEQ ID No. 795; SEQ ID No. 796; SEQ ID No. 797; SEQ ID No. 798; SEQ ID No. 799; SEQ ID No. 802; SEQ ID No. 803; SEQ ID
30 No. 806; SEQ ID No. 807; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 810; SEQ ID No. 811; SEQ ID No. 813; SEQ ID No. 814; SEQ ID No. 815; SEQ ID No. 816; SEQ ID No. 817; SEQ ID No. 819; SEQ ID No. 820; SEQ ID No. 821; SEQ ID No. 823; SEQ ID No. 824; SEQ ID No. 827; SEQ ID No. 829; SEQ ID No. 830; SEQ ID No. 831; SEQ ID No. 833; SEQ ID No. 834; SEQ ID No. 835; SEQ ID No. 837; SEQ ID No. 844; SEQ ID No. 845; SEQ ID No. 846; SEQ ID No. 847;
35 SEQ ID No. 848; SEQ ID No. 849; SEQ ID No. 850; SEQ ID No. 851; SEQ ID No. 852; SEQ ID No. 854; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 857; SEQ ID No. 859; SEQ ID No. 860; SEQ ID No. 862; SEQ ID No. 865; SEQ ID No. 866; SEQ ID No. 868; SEQ ID No. 869; SEQ ID

No. 870; SEQ ID No. 871; SEQ ID No. 872; SEQ ID No. 874; SEQ ID No. 877; SEQ ID No. 878; SEQ ID No. 879; SEQ ID No. 880; SEQ ID No. 881; SEQ ID No. 882; SEQ ID No. 884; SEQ ID No. 885; SEQ ID No. 888; SEQ ID No. 889; SEQ ID No. 890; SEQ ID No. 891; SEQ ID No. 892; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 896; SEQ ID No. 897; SEQ ID No. 899; 5 SEQ ID No. 900; SEQ ID No. 902; SEQ ID No. 903; SEQ ID No. 904; SEQ ID No. 905; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 912; SEQ ID No. 913; SEQ ID No. 914; SEQ ID No. 915; SEQ ID No. 917; SEQ ID No. 918; SEQ ID No. 919; SEQ ID No. 921; SEQ ID No. 923; SEQ ID No. 924; SEQ ID No. 926; SEQ ID No. 927; SEQ ID No. 928; SEQ ID No. 929; SEQ ID No. 930; SEQ ID No. 931; SEQ ID No. 937; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 941; SEQ ID 10 No. 943; SEQ ID No. 948; SEQ ID No. 951; SEQ ID No. 952; SEQ ID No. 953; SEQ ID No. 958; SEQ ID No. 960; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 968; SEQ ID No. 970; SEQ ID No. 974; SEQ ID No. 975; SEQ ID No. 977; SEQ ID No. 979; SEQ ID No. 980; SEQ ID No. 981; SEQ ID No. 983; SEQ ID No. 984; SEQ ID No. 985; SEQ ID No. 987; SEQ ID No. 989; SEQ ID No. 992; SEQ ID No. 993; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 999; 15 SEQ ID No. 1001; SEQ ID No. 1002; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1009; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1016; SEQ ID No. 1019; SEQ ID No. 1021; SEQ ID No. 1023; SEQ ID No. 1024; SEQ ID No. 1029; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1039; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1045; SEQ ID No. 1047; SEQ ID No. 1049; SEQ ID No. 1051; SEQ ID No. 1052; 20 SEQ ID No. 1053; SEQ ID No. 1054; SEQ ID No. 1056; SEQ ID No. 1059; SEQ ID No. 1061; SEQ ID No. 1062; SEQ ID No. 1063; SEQ ID No. 1064; SEQ ID No. 1065; SEQ ID No. 1067; SEQ ID No. 1075; SEQ ID No. 1077; SEQ ID No. 1078; SEQ ID No. 1079; SEQ ID No. 1080; SEQ ID No. 1081; SEQ ID No. 1089; SEQ ID No. 1095; SEQ ID No. 1097; SEQ ID No. 1098; SEQ ID No. 1099; SEQ ID No. 1101; SEQ ID No. 1102; SEQ ID No. 1103; SEQ ID No. 1106; 25 SEQ ID No. 1107; SEQ ID No. 1108; SEQ ID No. 1109; SEQ ID No. 1110; SEQ ID No. 1113; SEQ ID No. 1116; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1121; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1126; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131; SEQ ID No. 1133; SEQ ID No. 1134; SEQ ID No. 1136; SEQ ID No. 1137 and one of their representative fragments.

30 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its respective fragments, having between 4 and 6 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 5; SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 15; SEQ ID No. 36; SEQ ID No. 38; 35 SEQ ID No. 51; SEQ ID No. 55; SEQ ID No. 58; SEQ ID No. 67; SEQ ID No. 70; SEQ ID No. 81; SEQ ID No. 97; SEQ ID No. 110; SEQ ID No. 111; SEQ ID No. 115; SEQ ID No. 119; SEQ ID No. 126; SEQ ID No. 128; SEQ ID No. 148; SEQ ID No. 155; SEQ ID No. 163; SEQ ID

No. 165; SEQ ID No. 168; SEQ ID No. 169; SEQ ID No. 171; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 177; SEQ ID No. 181; SEQ ID No. 193; SEQ ID No. 203; SEQ ID No. 213; SEQ ID No. 214; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 221; SEQ ID No. 222; SEQ ID No. 225; SEQ ID No. 229; SEQ ID No. 243; SEQ ID No. 246; SEQ ID No. 248; SEQ ID No. 254; 5 SEQ ID No. 261; SEQ ID No. 285; SEQ ID No. 288; SEQ ID No. 292; SEQ ID No. 296; SEQ ID No. 298; SEQ ID No. 299; SEQ ID No. 301; SEQ ID No. 303; SEQ ID No. 317; SEQ ID No. 328; SEQ ID No. 329; SEQ ID No. 351; SEQ ID No. 354; SEQ ID No. 355; SEQ ID No. 364; SEQ ID No. 371; SEQ ID No. 374; SEQ ID No. 375; SEQ ID No. 391; SEQ ID No. 395; SEQ ID No. 401; SEQ ID No. 403; SEQ ID No. 405; SEQ ID No. 409; SEQ ID No. 414; SEQ ID No. 419; SEQ ID 10 No. 421; SEQ ID No. 423; SEQ ID No. 425; SEQ ID No. 438; SEQ ID No. 448; SEQ ID No. 453; SEQ ID No. 458; SEQ ID No. 466; SEQ ID No. 468; SEQ ID No. 470; SEQ ID No. 480; SEQ ID No. 489; SEQ ID No. 490; SEQ ID No. 496; SEQ ID No. 501; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 511; SEQ ID No. 513; SEQ ID No. 519; SEQ ID No. 526; SEQ ID No. 532; SEQ ID No. 538; SEQ ID No. 539; SEQ ID No. 547; SEQ ID No. 550; SEQ ID No. 561; 15 SEQ ID No. 568; SEQ ID No. 570; SEQ ID No. 574; SEQ ID No. 578; SEQ ID No. 579; SEQ ID No. 580; SEQ ID No. 582; SEQ ID No. 589; SEQ ID No. 593; SEQ ID No. 598; SEQ ID No. 601; SEQ ID No. 604; SEQ ID No. 610; SEQ ID No. 613; SEQ ID No. 617; SEQ ID No. 626; SEQ ID No. 632; SEQ ID No. 635; SEQ ID No. 638; SEQ ID No. 640; SEQ ID No. 641; SEQ ID No. 646; SEQ ID No. 649; SEQ ID No. 650; SEQ ID No. 651; SEQ ID No. 686; SEQ ID No. 711; SEQ ID 20 No. 724; SEQ ID No. 732; SEQ ID No. 734; SEQ ID No. 744; SEQ ID No. 745; SEQ ID No. 749; SEQ ID No. 751; SEQ ID No. 769; SEQ ID No. 770; SEQ ID No. 771; SEQ ID No. 773; SEQ ID No. 776; SEQ ID No. 779; SEQ ID No. 780; SEQ ID No. 785; SEQ ID No. 787; SEQ ID No. 789; SEQ ID No. 801; SEQ ID No. 805; SEQ ID No. 812; SEQ ID No. 822; SEQ ID No. 825; SEQ ID No. 826; SEQ ID No. 839; SEQ ID No. 841; SEQ ID No. 843; SEQ ID No. 853; SEQ ID No. 861; 25 SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 886; SEQ ID No. 893; SEQ ID No. 898; SEQ ID No. 906; SEQ ID No. 907; SEQ ID No. 908; SEQ ID No. 920; SEQ ID No. 922; SEQ ID No. 925; SEQ ID No. 933; SEQ ID No. 935; SEQ ID No. 936; SEQ ID No. 944; SEQ ID No. 946; SEQ ID No. 947; SEQ ID No. 954; SEQ ID No. 959; SEQ ID No. 961; SEQ ID No. 966; SEQ ID No. 967; SEQ ID No. 972; SEQ ID No. 978; SEQ ID No. 995; SEQ ID No. 996; SEQ ID No. 1000; SEQ ID 30 No. 1003; SEQ ID No. 1010; SEQ ID No. 1011; SEQ ID No. 1012; SEQ ID No. 1017; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1036; SEQ ID No. 1038; SEQ ID No. 1043; SEQ ID No. 1046; SEQ ID No. 1048; SEQ ID No. 1050; SEQ ID No. 1058; SEQ ID No. 1071; SEQ ID No. 1073; SEQ ID No. 1084; SEQ ID No. 1085; SEQ ID No. 1086; SEQ ID No. 1087; SEQ ID No. 1091; SEQ ID No. 1092; SEQ ID No. 1094; SEQ ID No. 1096; SEQ ID No. 1100; SEQ ID 35 No. 1104; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1117; SEQ ID No. 1122; SEQ ID No. 1125 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,

characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having at least 7 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 17; SEQ ID No. 52; SEQ ID No. 68; SEQ ID No. 83; SEQ ID No. 87; SEQ ID No. 109;
 5 SEQ ID No. 112; SEQ ID No. 113; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 127; SEQ ID
 No. 153; SEQ ID No. 204; SEQ ID No. 211; SEQ ID No. 218; SEQ ID No. 223; SEQ ID No. 275;
 SEQ ID No. 277; SEQ ID No. 295; SEQ ID No. 300; SEQ ID No. 302; SEQ ID No. 306; SEQ ID
 No. 327; SEQ ID No. 335; SEQ ID No. 342; SEQ ID No. 343; SEQ ID No. 347; SEQ ID No. 349;
 SEQ ID No. 361; SEQ ID No. 363; SEQ ID No. 369; SEQ ID No. 380; SEQ ID No. 388; SEQ ID
 10 No. 389; SEQ ID No. 397; SEQ ID No. 415; SEQ ID No. 432; SEQ ID No. 439; SEQ ID No. 446;
 SEQ ID No. 449; SEQ ID No. 472; SEQ ID No. 478; SEQ ID No. 500; SEQ ID No. 522; SEQ ID
 No. 524; SEQ ID No. 567; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 606; SEQ ID No. 609;
 SEQ ID No. 636; SEQ ID No. 639; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 668; SEQ ID
 No. 692; SEQ ID No. 702; SEQ ID No. 704; SEQ ID No. 713; SEQ ID No. 720; SEQ ID No. 778;
 15 SEQ ID No. 784; SEQ ID No. 800; SEQ ID No. 836; SEQ ID No. 838; SEQ ID No. 842; SEQ ID
 No. 864; SEQ ID No. 867; SEQ ID No. 883; SEQ ID No. 901; SEQ ID No. 916; SEQ ID No. 932;
 SEQ ID No. 934; SEQ ID No. 940; SEQ ID No. 942; SEQ ID No. 950; SEQ ID No. 956; SEQ ID
 No. 971; SEQ ID No. 973; SEQ ID No. 976; SEQ ID No. 988; SEQ ID No. 994; SEQ ID No. 1018;
 SEQ ID No. 1028; SEQ ID No. 1035; SEQ ID No. 1037; SEQ ID No. 1044; SEQ ID No. 1055;
 20 SEQ ID No. 1057; SEQ ID No. 1068; SEQ ID No. 1069; SEQ ID No. 1070; SEQ ID No. 1072;
 SEQ ID No. 1082; SEQ ID No. 1088; SEQ ID No. 1105; SEQ ID No. 1132; SEQ ID No. 1135 and
 one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a
Chlamydia pneumoniae surface exposed polypeptide or one of its representative fragments, and in that
 25 it is chosen from the polypeptides having the following sequences:

SEQ ID No. 15, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29,
 SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32, SEQ ID No. 33, SEQ ID No. 35, SEQ ID No. 36,
 SEQ ID No. 1257, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 314, SEQ ID No. 354, SEQ ID
 No. 380, SEQ ID No. 1266, SEQ ID No. 466, SEQ ID No. 467, SEQ ID No. 468, SEQ ID No. 469,
 30 SEQ ID No. 470, SEQ ID No. 472, SEQ ID No. 474, SEQ ID No. 476, SEQ ID No. 477, SEQ ID No.
 478, SEQ ID No. 479, SEQ ID No. 480, SEQ ID No. 482, SEQ ID No. 483, SEQ ID No. 485, SEQ ID
 No. 486, SEQ ID No. 500, SEQ ID No. 501, SEQ ID No. 503, SEQ ID No. 504, SEQ ID No. 505,
 SEQ ID No. 506, SEQ ID No. 507, SEQ ID No. 1268, SEQ ID No. 1269, SEQ ID No. 543, SEQ ID
 No. 544, SEQ ID No. 578, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 595,
 35 SEQ ID No. 596, SEQ ID No. 597, SEQ ID No. 1271, SEQ ID No. 633, SEQ ID No. 637, SEQ ID
 No. 699, SEQ ID No. 706, SEQ ID No. 737, SEQ ID No. 744, SEQ ID No. 1273, SEQ ID No. 751,
 SEQ ID No. 775, SEQ ID No. 776, SEQ ID No. 777, SEQ ID No. 793, SEQ ID No. 815, SEQ ID No.

830, SEQ ID No. 1221, SEQ ID No. 849, SEQ ID No. 851, SEQ ID No. 852, SEQ ID No. 874, SEQ ID No. 891, SEQ ID No. 922, SEQ ID No. 940, SEQ ID No. 1231, SEQ ID No. 1281, SEQ ID No. 1035, SEQ ID No. 1079, SEQ ID No. 1087, SEQ ID No. 1108, and one of their representative fragments.

- 5 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* lipoprotein or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:
- SEQ ID No. 3, SEQ ID No. 10, SEQ ID No. 11, SEQ ID No. 16, SEQ ID No. 1254, SEQ ID No. 1255, SEQ ID No. 38, SEQ ID No. 1256, SEQ ID No. 62, SEQ ID No. 85, SEQ ID No. 1258, SEQ ID
- 10 No. 115, SEQ ID No. 1151, SEQ ID No. 151, SEQ ID No. 1259, SEQ ID No. 173, SEQ ID No. 1261, SEQ ID No. 186, SEQ ID No. 194, SEQ ID No. 205, SEQ ID No. 214, SEQ ID No. 216, SEQ ID No. 217, SEQ ID No. 238, SEQ ID No. 1177, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 317, SEQ ID No. 327, SEQ ID No. 354, SEQ ID No. 364, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 432, SEQ ID No. 1192, SEQ ID No. 460, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 520, SEQ ID
- 15 No. 536, SEQ ID No. 1270, SEQ ID No. 576, SEQ ID No. 597, SEQ ID No. 603, SEQ ID No. 609, SEQ ID No. 637, SEQ ID No. 1272, SEQ ID No. 652, SEQ ID No. 1213, SEQ ID No. 699, SEQ ID No. 705, SEQ ID No. 706, SEQ ID No. 708, SEQ ID No. 711, SEQ ID No. 727, SEQ ID No. 1274, SEQ ID No. 800, SEQ ID No. 814, SEQ ID No. 825, SEQ ID No. 829, SEQ ID No. 830, SEQ ID No. 831, SEQ ID No. 844, SEQ ID No. 849, SEQ ID No. 1275, SEQ ID No. 1276, SEQ ID No. 1277, SEQ
- 20 ID No. 872, SEQ ID No. 878, SEQ ID No. 880, SEQ ID No. 891, SEQ ID No. 892, SEQ ID No. 1278, SEQ ID No. 1279, SEQ ID No. 1280, SEQ ID No. 941, SEQ ID No. 942, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 952, SEQ ID No. 988, SEQ ID No. 998, SEQ ID No. 1009, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1028, SEQ ID No. 1056, SEQ ID No. 1070, SEQ ID No. 1287, SEQ ID No. 1087, SEQ ID No. 1288, SEQ ID No. 1289, SEQ ID No. 1098, SEQ ID No. 1246, SEQ ID No.
- 25 1291, SEQ ID No. 1108, SEQ ID No. 1109, SEQ ID No. 1112, SEQ ID No. 1133, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, and in that it is chosen from the polypeptides having the following sequences:

- 30 SEQ ID No. 316, SEQ ID No. 564, SEQ ID No. 610, SEQ ID No. 647, SEQ ID No. 1211, SEQ ID No. 688, SEQ ID No. 924, and one of their representative fragments.

Preferably, the invention relates to additional LPS-related polypeptides according to the invention, in that it is:

- (a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octylosonic acid)-related
- 35 polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 177, SEQ ID No. 1156, SEQ ID No. 245, SEQ ID No. 767, and one of their representative fragments;

(b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 74, and its representative fragment;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1286, SEQ ID No. 1039, and its representative fragment; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 689, SEQ ID No. 690, SEQ ID No. 691, SEQ ID No. 1037, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence and is also an outer membrane protein, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 468 and its representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence that shows homology to *cds1*, *cds2*, and *copN* type III virulence loci in *Chlamydia Psitacci*, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 350 and its representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that is cysteine-rich and contains RGD sequence, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1290, SEQ ID No. 6846, SEQ ID No. 6848, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* outer membrane polypeptide that contains cysteines in their first 30 amino acids and also contain an RGD sequence, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 105, SEQ ID No. 106, SEQ ID No. 114, SEQ ID No. 170, SEQ ID No. 171, SEQ ID No. 1264, SEQ ID No. 268, SEQ ID No. 1265, SEQ ID No. 350, SEQ ID No. 393, SEQ ID No. 394, SEQ ID No. 451, SEQ ID No. 452, SEQ ID No. 453, SEQ ID No. 473, SEQ ID No. 499, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 525, SEQ ID No. 526, SEQ ID No. 538, SEQ ID No. 611, SEQ ID No. 645, SEQ ID No. 686, SEQ ID No. 700, SEQ ID No. 746, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No. 789, SEQ ID No. 814, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 878, SEQ ID No. 957, SEQ ID No. 958, SEQ ID No. 989, SEQ ID No. 1290, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a

Chlamydia pneumoniae polypeptide or one of its representative fragments that contains RGD sequences homologous to *Chlamydia trachomatis* polypeptides containing RGD sequences, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 114, SEQ ID No. 468, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 905, SEQ ID No. 913, SEQ ID No. 914, SEQ ID No. 915, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* Type III and non-Type III secreted polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

10 SEQ ID No. 25, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 33, SEQ ID No. 308, SEQ ID No. 309, SEQ ID No. 343, SEQ ID No. 344, SEQ ID No. 345, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 415, SEQ ID No. 480, SEQ ID No. 550, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 597, SEQ ID No. 699, SEQ ID No. 744, SEQ ID No. 751, SEQ ID No. 776, SEQ ID No. 866, SEQ ID No. 874, SEQ ID No. 883, SEQ ID No. 884, SEQ ID No. 888, SEQ ID No. 891, SEQ ID No. 6845, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 267, SEQ ID No. 271, SEQ ID No. 419, SEQ ID No. 590, SEQ ID No. 932, SEQ ID No. 6844, SEQ ID No. 6847, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments not found in *Chlamydia trachomatis* (Blastp $P > e^{-10}$), and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 7, SEQ ID No. 8, SEQ ID No. 9, SEQ ID No. 16, SEQ ID No. 17, SEQ ID No. 18, SEQ ID No. 19, SEQ ID No. 20, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 1254, SEQ ID No. 23, SEQ ID No. 1255, SEQ ID No. 24, SEQ ID No. 1139, SEQ ID No. 1140, SEQ ID No. 46, SEQ ID No. 47, SEQ ID No. 51, SEQ ID No. 60, SEQ ID No. 1256, SEQ ID No. 61, SEQ ID No. 62, SEQ ID No. 63, SEQ ID No. 64, SEQ ID No. 1257, SEQ ID No. 65, SEQ ID No. 66, SEQ ID No. 67, SEQ ID No. 68, 30 SEQ ID No. 1143, SEQ ID No. 1145, SEQ ID No. 83, SEQ ID No. 84, SEQ ID No. 1146, SEQ ID No. 85, SEQ ID No. 86, SEQ ID No. 87, SEQ ID No. 1258, SEQ ID No. 116, SEQ ID No. 117, SEQ ID No. 125, SEQ ID No. 1148, SEQ ID No. 143, SEQ ID No. 1150, SEQ ID No. 1151, SEQ ID No. 144, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 148, SEQ ID No. 149, SEQ ID No. 150, SEQ ID No. 152, SEQ ID No. 1259, SEQ ID No. 162, SEQ ID No. 166, SEQ ID No. 1154, SEQ ID No. 167, 35 SEQ ID No. 1261, SEQ ID No. 1156, SEQ ID No. 1157, SEQ ID No. 178, SEQ ID No. 179, SEQ ID No. 1158, SEQ ID No. 182, SEQ ID No. 183, SEQ ID No. 184, SEQ ID No. 185, SEQ ID No. 1159, SEQ ID No. 186, SEQ ID No. 1160, SEQ ID No. 187, SEQ ID No. 188, SEQ ID No. 189, SEQ ID

No. 190, SEQ ID No. 1161, SEQ ID No. 1162, SEQ ID No. 191, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 195, SEQ ID No. 1163, SEQ ID No. 196, SEQ ID No. 201, SEQ ID No. 202, SEQ ID No. 209, SEQ ID No. 212, SEQ ID No. 221, SEQ ID No. 224, SEQ ID No. 1167, SEQ ID No. 226, SEQ ID No. 227, SEQ ID No. 228, SEQ ID No. 229, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 1169, SEQ ID No. 1170, SEQ ID No. 1171, SEQ ID No. 234, SEQ ID No. 235, SEQ ID No. 236, SEQ ID No. 1172, SEQ ID No. 243, SEQ ID No. 251, SEQ ID No. 252, SEQ ID No. 1176, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 1177, SEQ ID No. 1178, SEQ ID No. 262, SEQ ID No. 263, SEQ ID No. 1264, SEQ ID No. 278, SEQ ID No. 279, SEQ ID No. 1180, SEQ ID No. 280, SEQ ID No. 290, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 296, SEQ ID No. 1181, SEQ ID No. 297, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 1265, SEQ ID No. 322, SEQ ID No. 324, SEQ ID No. 325, SEQ ID No. 370, SEQ ID No. 1186, SEQ ID No. 371, SEQ ID No. 372, SEQ ID No. 1187, SEQ ID No. 373, SEQ ID No. 378, SEQ ID No. 1266, SEQ ID No. 382, SEQ ID No. 383, SEQ ID No. 384, SEQ ID No. 385, SEQ ID No. 386, SEQ ID No. 1188, SEQ ID No. 1189, SEQ ID No. 391, SEQ ID No. 392, SEQ ID No. 398, SEQ ID No. 400, SEQ ID No. 403, SEQ ID No. 1191, SEQ ID No. 423, SEQ ID No. 435, SEQ ID No. 445, SEQ ID No. 450, SEQ ID No. 1193, SEQ ID No. 456, SEQ ID No. 460, SEQ ID No. 461, SEQ ID No. 465, SEQ ID No. 1196, SEQ ID No. 471, SEQ ID No. 473, SEQ ID No. 475, SEQ ID No. 481, SEQ ID No. 484, SEQ ID No. 487, SEQ ID No. 488, SEQ ID No. 489, SEQ ID No. 490, SEQ ID No. 491, SEQ ID No. 492, SEQ ID No. 493, SEQ ID No. 494, SEQ ID No. 495, SEQ ID No. 496, SEQ ID No. 497, SEQ ID No. 498, SEQ ID No. 499, SEQ ID No. 502, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 508, SEQ ID No. 510, SEQ ID No. 509, SEQ ID No. 512, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 1197, SEQ ID No. 521, SEQ ID No. 1198, SEQ ID No. 522, SEQ ID No. 524, SEQ ID No. 528, SEQ ID No. 534, SEQ ID No. 537, SEQ ID No. 1269, SEQ ID No. 1270, SEQ ID No. 548, SEQ ID No. 551, SEQ ID No. 557, SEQ ID No. 1201, SEQ ID No. 1203, SEQ ID No. 562, SEQ ID No. 566, SEQ ID No. 593, SEQ ID No. 595, SEQ ID No. 600, SEQ ID No. 1271, SEQ ID No. 604, SEQ ID No. 611, SEQ ID No. 612, SEQ ID No. 614, SEQ ID No. 616, SEQ ID No. 625, SEQ ID No. 627, SEQ ID No. 628, SEQ ID No. 629, SEQ ID No. 631, SEQ ID No. 641, SEQ ID No. 1272, SEQ ID No. 648, SEQ ID No. 1212, SEQ ID No. 663, SEQ ID No. 685, SEQ ID No. 707, SEQ ID No. 714, SEQ ID No. 715, SEQ ID No. 716, SEQ ID No. 717, SEQ ID No. 722, SEQ ID No. 746, SEQ ID No. 1273, SEQ ID No. 761, SEQ ID No. 764, SEQ ID No. 770, SEQ ID No. 1217, SEQ ID No. 783, SEQ ID No. 1274, SEQ ID No. 803, SEQ ID No. 815, SEQ ID No. 1220, SEQ ID No. 835, SEQ ID No. 1221, SEQ ID No. 844, SEQ ID No. 845, SEQ ID No. 846, SEQ ID No. 847, SEQ ID No. 848, SEQ ID No. 849, SEQ ID No. 850, SEQ ID No. 851, SEQ ID No. 1275, SEQ ID No. 852, SEQ ID No. 862, SEQ ID No. 1276, SEQ ID No. 1277, SEQ ID No. 873, SEQ ID No. 1223, SEQ ID No. 892, SEQ ID No. 919, SEQ ID No. 1225, SEQ ID No. 1278, SEQ ID No. 926, SEQ ID No. 1228, SEQ ID No. 1229, SEQ ID No. 1230, SEQ ID No. 1279, SEQ ID No. 1281, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 948, SEQ ID No. 950, SEQ ID No. 949, SEQ ID No. 951, SEQ ID No. 980, SEQ ID No.

982, SEQ ID No. 1233, SEQ ID No. 999, SEQ ID No. 1000, SEQ ID No. 1001, SEQ ID No. 1002, SEQ ID No. 1008, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1016, SEQ ID No. 1019, SEQ ID No. 1027, SEQ ID No. 1036, SEQ ID No. 1241, SEQ ID No. 1048, SEQ ID No. 1049, SEQ ID No. 1050, SEQ ID No. 1053, SEQ ID No. 1054, SEQ ID No. 1064, SEQ ID No. 1076, SEQ ID No. 1091, 5 SEQ ID No. 1288, SEQ ID No. 1093, SEQ ID No. 1289, SEQ ID No. 1101, SEQ ID No. 1103, SEQ ID No. 1245, SEQ ID No. 1246, SEQ ID No. 1247, SEQ ID No. 1290, SEQ ID No. 1291, SEQ ID No. 1115, SEQ ID No. 1116, SEQ ID No. 1118, SEQ ID No. 1120, SEQ ID No. 1249, SEQ ID No. 1121, SEQ ID No. 1250, SEQ ID No. 1126, SEQ ID No. 1251, SEQ ID No. 1127, SEQ ID No. 1128, SEQ ID No. 1130, SEQ ID No. 1129, SEQ ID No. 1131, SEQ ID No. 1136, SEQ ID No. 1253, SEQ ID No. 10 6844, SEQ ID No. 6846, SEQ ID No. 6847, SEQ ID No. 6848, and one of their representative fragments

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of 15 cofactors, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 55; SEQ ID No. 56; SEQ ID No. 69; SEQ ID No. 75; SEQ ID No. 80; SEQ ID No. 100; SEQ ID No. 110; SEQ ID No. 114; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 157; SEQ ID No. 160; SEQ ID No. 161; SEQ ID No. 172; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 198; SEQ ID No. 200; SEQ ID No. 225; SEQ ID No. 248; SEQ ID No. 249; SEQ ID 20 No. 276; SEQ ID No. 277; SEQ ID No. 318; SEQ ID No. 319; SEQ ID No. 320; SEQ ID No. 323; SEQ ID No. 331; SEQ ID No. 347; SEQ ID No. 375; SEQ ID No. 376; SEQ ID No. 381; SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 395; SEQ ID No. 396; SEQ ID No. 409; SEQ ID No. 446; SEQ ID No. 447; SEQ ID No. 448; SEQ ID No. 449; SEQ ID No. 513; SEQ ID No. 516; SEQ ID No. 571; SEQ ID No. 647; SEQ ID No. 662; SEQ ID No. 697; SEQ ID No. 718; SEQ ID No. 793; 25 SEQ ID No. 794; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 838; SEQ ID No. 839; SEQ ID No. 840; SEQ ID No. 853; SEQ ID No. 854; SEQ ID No. 918; SEQ ID No. 923; SEQ ID No. 929; SEQ ID No. 931; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 958; SEQ ID No. 959; SEQ ID No. 960; SEQ ID No. 966; SEQ ID No. 995; SEQ ID No. 1021; SEQ ID No. 1040; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1085; SEQ ID No. 1100; SEQ ID No. 1102; SEQ ID 30 No. 1117; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1120; SEQ ID No. 1135 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, and in that it is 35 chosen from the polypeptides having the following sequences:

SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 138; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 233; SEQ ID No. 246; SEQ ID No. 338; SEQ ID No. 412; SEQ ID No. 421; SEQ ID No. 438;

SEQ ID No. 607; SEQ ID No. 648; SEQ ID No. 657; SEQ ID No. 740; SEQ ID No. 783; SEQ ID No. 967; SEQ ID No. 989; SEQ ID No. 990; SEQ ID No. 992; SEQ ID No. 1011; SEQ ID No. 1058; SEQ ID No. 1059; SEQ ID No. 1073; SEQ ID No. 1074 and one of their representative fragments.

5 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 14; SEQ ID No. 59; SEQ ID No. 70; SEQ ID No. 71; SEQ ID No. 97; SEQ ID
10 No. 113; SEQ ID No. 137; SEQ ID No. 141; SEQ ID No. 169; SEQ ID No. 285; SEQ ID No. 287;
SEQ ID No. 288; SEQ ID No. 313; SEQ ID No. 326; SEQ ID No. 358; SEQ ID No. 411; SEQ ID
No. 443; SEQ ID No. 548; SEQ ID No. 569; SEQ ID No. 601; SEQ ID No. 651; SEQ ID No. 654;
SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 694; SEQ ID
No. 698; SEQ ID No. 704; SEQ ID No. 760; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 786;
15 SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 801; SEQ ID No. 802; SEQ ID No. 812; SEQ ID
No. 819; SEQ ID No. 822; SEQ ID No. 870; SEQ ID No. 897; SEQ ID No. 898; SEQ ID No. 902;
SEQ ID No. 908; SEQ ID No. 916; SEQ ID No. 954; SEQ ID No. 955; SEQ ID No. 961; SEQ ID
No. 983; SEQ ID No. 996; SEQ ID No. 1007; SEQ ID No. 1012; SEQ ID No. 1013; SEQ ID
No. 1014; SEQ ID No. 1015; SEQ ID No. 1038; SEQ ID No. 1137 and one of their representative
20 fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of amino acids or polypeptides, and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 99; SEQ ID No. 111; SEQ ID No. 127; SEQ ID No. 134; SEQ ID No. 140; SEQ ID
No. 174; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 353; SEQ ID No. 377; SEQ ID No. 404;
SEQ ID No. 523; SEQ ID No. 539; SEQ ID No. 559; SEQ ID No. 561; SEQ ID No. 586; SEQ ID
No. 598; SEQ ID No. 609; SEQ ID No. 636; SEQ ID No. 687; SEQ ID No. 700; SEQ ID No. 701;
SEQ ID No. 759; SEQ ID No. 790; SEQ ID No. 857; SEQ ID No. 861; SEQ ID No. 904; SEQ ID
30 No. 936; SEQ ID No. 952; SEQ ID No. 962; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965;
SEQ ID No. 991; SEQ ID No. 1003; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1018;
SEQ ID No. 1067; SEQ ID No. 1110; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114;
SEQ ID No. 1121; SEQ ID No. 1122; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1125 and
one of their representative fragments.

35 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of polypeptides, and in that it is chosen from the polypeptides

having the following sequences:

SEQ ID No. 4; SEQ ID No. 44; SEQ ID No. 45; SEQ ID No. 48; SEQ ID No. 54; SEQ ID No. 112; SEQ ID No. 130; SEQ ID No. 155; SEQ ID No. 163; SEQ ID No. 212; SEQ ID No. 257; SEQ ID No. 307; SEQ ID No. 343; SEQ ID No. 405; SEQ ID No. 416; SEQ ID No. 458; SEQ ID
 5 No. 540; SEQ ID No. 541; SEQ ID No. 542; SEQ ID No. 543; SEQ ID No. 544; SEQ ID No. 560; SEQ ID No. 594; SEQ ID No. 652; SEQ ID No. 699; SEQ ID No. 723; SEQ ID No. 747; SEQ ID No. 817; SEQ ID No. 827; SEQ ID No. 871; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 911; SEQ ID No. 912; SEQ ID No. 1023; SEQ ID No. 1051; SEQ ID No. 1052; SEQ ID No. 1081 and one of their representative fragments.

10 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of fatty acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 76; SEQ ID No. 284; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID
 15 No. 311; SEQ ID No. 312; SEQ ID No. 425; SEQ ID No. 433; SEQ ID No. 565; SEQ ID No. 688; SEQ ID No. 690; SEQ ID No. 691; SEQ ID No. 767; SEQ ID No. 797; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 994; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1046; SEQ ID No. 1047; SEQ ID No. 1057 and one of their representative fragments.

20 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the synthesis of the wall, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 49; SEQ ID No. 50; SEQ ID No. 177; SEQ ID No. 178; SEQ ID No. 245; SEQ ID
 25 No. 610; SEQ ID No. 972; SEQ ID No. 974; SEQ ID No. 978; SEQ ID No. 1037 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, and in that it is chosen
 30 from the polypeptides having the following sequences:

SEQ ID No. 90; SEQ ID No. 92; SEQ ID No. 131; SEQ ID No. 151; SEQ ID No. 199; SEQ ID No. 333; SEQ ID No. 334; SEQ ID No. 336; SEQ ID No. 379; SEQ ID No. 589; SEQ ID No. 590; SEQ ID No. 619; SEQ ID No. 630; SEQ ID No. 649; SEQ ID No. 739; SEQ ID No. 741; SEQ ID No. 806; SEQ ID No. 821; SEQ ID No. 843; SEQ ID No. 968; SEQ ID No. 971; SEQ ID No. 1061
 35 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative

fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 93; SEQ ID No. 94; SEQ ID No. 95; SEQ ID No. 136; SEQ ID No. 259; SEQ ID No. 332; SEQ ID No. 348; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 663; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 669; SEQ ID
5 No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 675; SEQ ID No. 676; SEQ ID No. 677; SEQ ID No. 678; SEQ ID No. 679; SEQ ID No. 680; SEQ ID No. 681; SEQ ID No. 683; SEQ ID No. 684; SEQ ID No. 738; SEQ ID No. 781; SEQ ID No. 1008; SEQ ID No. 1024; SEQ ID No. 1025; SEQ ID No. 1066 and one of their representative fragments.

Preferably, the invention also relates to a polypeptide according to the invention,
10 characterized in that it is a *Chlamydia pneumoniae* transport polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 40; SEQ ID No. 41; SEQ ID No. 52; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107; SEQ ID No. 109; SEQ ID No. 133; SEQ ID No. 210; SEQ ID No. 211; SEQ ID No. 214; SEQ ID No. 215; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 218; SEQ ID No. 219; SEQ ID
15 No. 220; SEQ ID No. 223; SEQ ID No. 242; SEQ ID No. 260; SEQ ID No. 293; SEQ ID No. 299; SEQ ID No. 366; SEQ ID No. 369; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 638; SEQ ID No. 639; SEQ ID No. 640; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 702; SEQ ID No. 703; SEQ ID No. 724; SEQ ID No. 732; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 901; SEQ ID No. 906; SEQ ID No. 933; SEQ ID No. 942; SEQ ID No. 1043; SEQ ID No. 1086; SEQ ID
20 No. 1105 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the virulence process, and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 546; SEQ ID No. 550; SEQ ID No. 778; SEQ ID No. 779; SEQ ID No. 886 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, and in that it is chosen from the
30 polypeptides having the following sequences:

SEQ ID No. 751; SEQ ID No. 874; SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 883; SEQ ID No. 884; SEQ ID No. 885 and one of their representative fragments.

The secreted polypeptides, including the Type III and other, non-Type III secreted polypeptides, of the present invention, as well as the corresponding nucleotide sequences, may be
35 detected by techniques known to persons skilled in the art, such as for example the techniques using cloning combined with vectors allowing the expression of the said polypeptides fused to export markers such as the *luc* gene for luciferase or the *PhoA* gene for alkaline phosphatase.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments (with a Blast E value of $>10^{-5}$), and in that it is chosen from the polypeptides having the following sequences:

- 5 SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 17; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20; SEQ ID No. 22; SEQ ID No. 23; SEQ ID No. 24; SEQ ID No. 51; SEQ ID No. 60; SEQ ID No. 63; SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 67; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 87; SEQ ID No. 125; SEQ ID No. 143; SEQ ID No. 144; SEQ ID No. 179; SEQ ID No. 182; SEQ ID No. 184; SEQ ID No. 185; SEQ ID No. 187; SEQ ID No. 221;
10 SEQ ID No. 252; SEQ ID No. 254;; SEQ ID No. 278; SEQ ID No. 279; SEQ ID No. 387; SEQ ID No. 388; SEQ ID No. 397; SEQ ID No. 1048; SEQ ID No. 1049; SEQ ID No. 1050; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131 and one of their representative fragments.

- In general, in the present invention, the functional group to which a polypeptide of the invention belongs, as well as its corresponding nucleotide sequence, may be determined either by
15 comparative analogy with sequences already known, or by the use of standard techniques of biochemistry, of cytology combined with the techniques of genetic engineering such as immunoaffinity, localization by immunolabelling, differential extraction, measurement of enzymatic activity, study of the activity inducing or repressing expression or the study of expression in *E. coli*.

- It is clearly understood, on the one hand, that, in the present invention, the nucleotide
20 sequences (ORF) and the amino acid sequences (SEQ ID No. 2 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6848) which are listed by functional group, are not exhaustive within the group considered. Moreover, it is also clearly understood that, in the present invention, a nucleotide sequence (ORF) or an amino acid sequence mentioned within a given functional group may also be part of another group taking into account, for example, the interrelationship between the groups listed.
25 Accordingly, and as an example of this interrelationship, an exported and/or secreted polypeptide as well as its coding nucleotide sequence may also be involved in the *Chlamydia pneumoniae* virulence process by modifying the defense mechanism of the infected host cell, or a transmembrane polypeptide or its coding nucleotide sequence is also part of the polypeptides or coding nucleotide sequences of the cellular envelope.

- 30 The subject of the present invention is also the nucleotide and/or polypeptide sequences according to the invention, characterized in that the said sequences are recorded on a medium, called recording medium, whose type and nature facilitate the reading, the analysis and the exploitation of the said sequences. These media may of course also contain other information extracted from the present invention, such as in particular the analogies with already known sequences, such as those
35 mentioned in Table 1 of the present description, and/or may contain, in addition, information relating to the nucleotide and/or polypeptide sequences of other microorganisms so as to facilitate the comparative analysis and the exploitation of the results obtained.

Among these recording media, computer-readable media, such as magnetic, optical, electrical and hybrid media such as, for example, floppy disks, CD-ROMs or recording cassettes, are preferred in particular.

The invention also relates to nucleotide sequences which can be used as primer or probe, characterized in that the said sequences are chosen from the nucleotide sequences according to the invention.

The invention relates, in addition, to the use of a nucleotide sequence according to the invention, as primer or probe, for the detection and/or amplification of nucleic acid sequences.

The nucleotide sequences according to the invention may thus be used to amplify nucleotide sequences, in particular by the PCR technique (polymerase chain reaction) (Erich, 1989; Innis et al., 1990; Rolfs et al., 1991, and White et al., 1997).

These oligodeoxyribonucleotide or oligoribonucleotide primers correspond to representative nucleotide fragments, and are advantageously at least 8 nucleotides, preferably at least 12 nucleotides, 15 nucleotides and still more preferably at least 20 nucleotides long.

Other techniques for amplifying the target nucleic acid may be advantageously used as alternatives to PCR.

The nucleotide sequences of the invention, in particular the primers according to the invention, may also be used in other methods for amplifying a target nucleic acid, such as:

- the TAS (Transcription-based Amplification System) technique described by Kwoh et al. in 1989;
- the 3SR (Self-Sustained Sequence Replication) technique described by Guatelli et al. in 1990;
- the NASBA (Nucleic Acid Sequence Based Amplification) technique described by Kievitis et al. in 1991;
- the SDA (Strand Displacement Amplification) technique (Walker et al., 1992);
- the TMA (Transcription Mediated Amplification) technique.

The polynucleotides of the invention may also be used in techniques for amplifying or for modifying the nucleic acid serving as probe, such as:

- the LCR (Ligase Chain Reaction) technique described by Landegren et al. in 1988 and perfected by Barany et al. in 1991, which uses a thermostable ligase;
- the RCR (Repair Chain Reaction) technique described by Segev in 1992;
- the CPR (Cycling Probe Reaction) technique described by Duck et al. in 1990;
- the Q-beta-replicase amplification technique described by Miele et al. in 1983 and perfected in particular by Chu et al. in 1986, Lizardi et al. in 1988, and then by Burg et al. as well as by Stone et al. in 1996.

The invention also relates to the nucleotide sequences of fragments which can be obtained by amplification with the aid of at least one primer according to the invention. The present invention encompasses both hybridization probes and primers. In general, the complementary probes should be of a length sufficient to form a stable hybrid complex with the target sequences. Primers,

while complementary to the target sequences need not form stable hybridization complexes with the target sequences alone. Rather, primers form stable complexes with the target sequences in the presence of polymerase to permit extension of the primer.

In the case where the target polynucleotide to be detected is possibly an RNA, for example an mRNA, it will be possible to use, prior to the use of an amplification reaction with the aid of at least one primer according to the invention or to the use of a method of detection with the aid of at least one probe of the invention, a reverse transcriptase-type enzyme so as to obtain a cDNA from the RNA contained in the biological sample. The cDNA obtained will then serve as target for the primer(s) or the probe(s) used in the amplification or detection method according to the invention.

10 The detection probe will be chosen so that it hybridizes with the target sequence or the amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 12 nucleotides, in particular of at least 20 nucleotides, and preferably at least 100 nucleotides.

The invention also comprises the nucleotide sequences which can be used as probe or primer according to the invention, characterized in that they are labelled with a radioactive compound or with a nonradioactive compound.

The nonlabelled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labelled with a radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or with a nonradioactive molecule (biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, fluorescein) so as to obtain probes which can be used in numerous applications.

Examples of nonradioactive labelling of nucleotide sequences are described, for example, in French patent No. 78,10975 or by Urdea et al. or by Sanchez-Pescador et al. in 1988.

In the latter case, one of the labelling methods described in patents FR-2 422 956 and FR-2 518 755 may also be used.

25 The invention also relates to the nucleotide sequences of fragments which can be obtained by hybridization with the aid of at least one probe according to the invention.

The hybridization technique may be performed in various ways (Matthews et al., 1988). The most common method consists in immobilizing the nucleic acid extracted from *Chlamydia pneumoniae* cells on a support (such as nitrocellulose, nylon, polystyrene) and in incubating, under well-defined conditions, the target nucleic acid immobilized with the probe. After hybridization, the excess probe is removed and the hybrid molecules formed are detected by the appropriate method (measurement of the radioactivity, of the fluorescence or of the enzymatic activity linked to the probe).

35 The invention also comprises the nucleotide sequences according to the invention, characterized in that they are covalently or noncovalently immobilized on a support.

According to another advantageous embodiment of the nucleic sequences according to the invention, the latter may be used immobilized on a support and may thus serve to capture, through

specific hybridization, the target nucleic acid obtained from the biological sample to be tested. If necessary, the solid support is separated from the sample and the hybridization complex formed between the so-called capture probe and the target nucleic acid is then detected by means of a second probe, called detection probe, labelled with an easily detectable element.

5 The nucleotide sequences according to the invention may also be used in new analytical systems, DNA chips, which allow sequencing, the study of mutations and of the expression of genes, and which are currently of interest given their very small size and their high capacity in terms of number of analyses.

 The principle of the operation of these chips is based on molecular probes, most often
10 oligonucleotides, which are attached onto a miniaturized surface, generally of the order of a few square centimetres. During an analysis, a sample containing fragments of a target nucleic acid to be analysed, for example DNA or RNA labelled, for example, after amplification, is deposited onto the DNA chip in which the support has been coated beforehand with probes. Bringing the labelled target
15 sequences into contact with the probes leads to the formation, through hybridization, of a duplex according to the rule of pairing defined by J.D. Watson and F. Crick. After a washing step, analysis of the surface of the chip allows the effective hybridizations to be located by means of the signals emitted by the labels tagging the target. A hybridization fingerprint results from this analysis which, by appropriate computer processing, will make it possible to determine information such as the presence of specific fragments in the sample, the determination of sequences and the presence of mutations.

20 The chip consists of a multitude of molecular probes, precisely organized or arrayed on a solid support whose surface is miniaturized. It is at the centre of a system where other elements (imaging system, microcomputer) allow the acquisition and interpretation of a hybridization fingerprint.

 The hybridization supports are provided in the form of flat or porous surfaces (pierced
25 with wells) composed of various materials. The choice of a support is determined by its physicochemical properties, or more precisely, by the relationship between the latter and the conditions under which the support will be placed during the synthesis or the attachment of the probes or during the use of the chip. It is therefore necessary, before considering the use of a particular support (R.S. Matson et al., 1994), to consider characteristics such as its stability to pH, its physical
30 strength, its reactivity and its chemical stability as well as its capacity to nonspecifically bind nucleic acids. Materials such as glass, silicon and polymers are commonly used. Their surface is, in a first step, called "functionalization", made reactive towards the groups which it is desired to attach thereon. After the functionalization, so-called spacer molecules are grafted onto the activated surface. Used as intermediates between the surface and the probe, these molecules of variable size render unimportant
35 the surface properties of the supports, which often prove to be problematic for the synthesis or the attachment of the probes and for the hybridization.

 Among the hybridization supports, there may be mentioned glass which is used, for

example, in the method of in situ synthesis of oligonucleotides by photochemical addressing developed by the company Affymetrix (E.L. Sheldon, 1993), the glass surface being activated by silane. Genosensor Consortium (P. Mérel, 1994) also uses glass slides carrying wells 3 mm apart, this support being activated with epoxysilane.

5 Polymers or silicon may also be mentioned among these hybridization supports. For example, the Andrein Mirzabekov team has developed a chip consisting of polyacrylamide squares polymerized on a silanized glass surface (G. Yershov et al., 1996). Several teams use silicon, in particular the IFOS laboratory of Ecole Centrale of Lyon which uses a silicon semiconductor substrate which is p-doped by introducing it into its crystalline structure atoms whose valency is different from
10 that of silicon. Various types of metals, in particular gold and platinum, may also be used as support (Genosensor Consortium (K. Beattie et al., 1993)).

 The probes according to the invention may be synthesized directly in situ on the supports of the DNA chips. This in situ synthesis may be carried out by photochemical addressing (developed by the company Affymax (Amsterdam, Holland) and exploited industrially by its subsidiary
15 Affymetrix (United States)) or based on the VLSIPS (very large scale immobilized polymer synthesis) technology (S.P.A. Fodor et al., 1991) which is based on a method of photochemically directed combinatorial synthesis and the principle of which combines solid-phase chemistry, the use of photolabile protecting groups and photolithography.

 The probes according to the invention may be attached to the DNA chips in various ways
20 such as electrochemical addressing, automated addressing or the use of probe printers (T. Livache et al., 1994; G. Yershov et al., 1996; J. Derisi et al., 1996, and S. Borman, 1996).

 The revealing of the hybridization between the probes of the invention, deposited or synthesized in situ on the supports of the DNA chips, and the sample to be analysed, may be determined, for example, by measurement of fluorescent signals, by radioactive counting or by
25 electronic detection.

 The use of fluorescent molecules such as fluorescein constitutes the most common method of labelling the samples. It allows direct or indirect revealing of the hybridization and allows the use of various fluorochromes.

 Affymetrix currently provides an apparatus or a scanner designed to read its Gene Chip™
30 chips. It makes it possible to detect the hybridizations by scanning the surface of the chip in confocal microscopy (R.J. Lipshutz et al., 1995). Other methods of detecting fluorescent signals have been tested: coupling of an epifluorescence microscope and a CCD camera (G. Yershov et al., 1996), the use of an optical fibre collecting system (E.L. Sheldon, 1993). A conventional method consists in carrying out an end labelling, with phosphorus 32, of the target sequences, by means of an appropriate
35 apparatus, the Phosphorimager (marketed by Molecular Dynamics). The electronic detection is based on the principle that the hybridization of two nucleic acid molecules is accompanied by physical phenomena which can be quantified under certain conditions (system developed by Ecole Centrale of

Lyon and called GEN-FET (GEN field effect transistor)). Genosensor Consortium and the company Beckman Instruments who are developing an electronic chip or Permittivity Chips™ may also be mentioned (K. Beattie et al., 1993).

The nucleotide sequences according to the invention may thus be used in DNA chips to
5 carry out the analysis of mutations. This analysis is based on the production of chips capable of analysing each base of a nucleotide sequence according to the invention.

The nucleotide sequences according to the invention may also be used in DNA chips to carry out the analysis of the expression of the *Chlamydia pneumoniae* genes. This analysis of the expression of *Chlamydia pneumoniae* genes is based on the use of chips where probes of the
10 invention, chosen for their specificity to characterize a given gene, are present (D.J. Lockhart et al., 1996; D.D. Shoemaker et al., 1996). For the methods of analysis of gene expression using the DNA chips, reference may, for example, be made to the methods described by D.J. Lockhart et al. (1996) and Sosnowsky et al. (1997) for the synthesis of probes in situ or for the addressing and the attachment of previously synthesized probes. The target sequences to be analysed are labelled and in general
15 fragmented into sequences of about 50 to 100 nucleotides before being hybridized onto the chip. After washing as described, for example, by D.J. Lockhart et al. (1996) and application of different electric fields (Sosnowsky et al., 1997), the labelled compounds are detected and quantified, the hybridizations being carried out at least in duplicate. Comparative analyses of the signal intensities obtained with respect to the same probe for different samples and/or for different probes with the same sample,
20 determine the differential expression of RNA or of DNA derived from the sample.

The nucleotide sequences according to the invention may, in addition, be used in DNA chips where other nucleotide probes specific for other microorganisms are also present, and may allow the carrying out of a serial test allowing rapid identification of the presence of a microorganism in a sample.

25 Accordingly, the subject of the invention is also the nucleotide sequences according to the invention, characterized in that they are immobilized on a support of a DNA chip.

The DNA chips, characterized in that they contain at least one nucleotide sequence according to the invention, immobilized on the support of the said chip, also form part of the invention.

30 The said chips will preferably contain several probes or nucleotide sequences of the invention of different length and/or corresponding to different genes so as to identify, with greater certainty, the specificity of the target sequences or the desired mutation in the sample to be analysed.

Accordingly, the analyses carried out by means of primers and/or probes according to the invention, immobilized on supports such as DNA chips, will make it possible, for example, to identify,
35 in samples, mutations linked to variations such as intraspecies variations. These variations may be correlated or associated with pathologies specific to the variant identified and will make it possible to select the appropriate treatment.

The invention thus comprises a DNA chip according to the invention, characterized in that it contains, in addition, at least one nucleotide sequence of a microorganism different from *Chlamydia pneumoniae*, immobilized on the support of the said chip; preferably, the different microorganism will be chosen from an associated microorganism, a bacterium of the

5 *Chlamydia* family, and a variant of the species *Chlamydia pneumoniae*.

Another subject of the present invention is a vector for the cloning and/or the expression of a sequence, characterized in that it contains a nucleotide sequence according to the invention. Among the said vectors according to the invention, the vectors containing a nucleotide sequence encoding a polypeptide of the cellular, preferably outer, envelope of *Chlamydia pneumoniae* or one of

10 its representative fragments, are preferred. In a specific embodiment, the vectors contain a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide (LPS) biosynthesis, a Type III and non-Type III secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall

15 anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids

20 or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*.

According to the invention, the vectors comprise the elements necessary to allow the expression and/or the secretion of the said nucleotide sequences in a given host cell, and form part of the invention. The vector should, in this case, comprise a promoter, signals for initiation and for

25 termination of translation, as well as appropriate regions for regulation of transcription. It should be capable of being stably maintained in the host cell and may optionally possess particular signals specifying the secretion of the translated protein. These different elements are chosen according to the host cell used. To this effect, the nucleotide sequences according to the invention may be inserted into autonomously-replicating vectors within the chosen host, or integrative vectors in the chosen host.

30 Any of the standard methods known to those skilled in the art for the insertion of DNA fragments into a vector may be used to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinants (genetic recombination).

35 Expression of a polypeptide, peptide or derivative, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1 or ORFs contained within SEQ ID No. 1 may be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed

with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42); prokaryotic expression vectors such as the β -lactamase promoter (Villa-Kamaroff, *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella *et al.*, 1983, Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, *et al.*, 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella *et al.*, 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, Cell 38:639-646; Ornitz *et al.*, 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, Cell 38:647-658; Adames *et al.*, 1985, Nature 318:533-538; Alexander *et al.*, 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert *et al.*, 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf *et al.*, 1985, Mol. Cell. Biol. 5:1639-1648; Hammer *et al.*, 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver (Kelsey *et al.*, 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogam *et al.*, 1985, Nature 315:338-340; Kollias *et al.*, 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason *et al.*, 1986, Science 234:1372-1378).

The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a protein or peptide-encoding a nucleic acid sequence in SEQ ID No. 1, or ORFs contained within SEQ ID No. 1, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an

antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Preferred vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen). Furthermore, the vectors according to the invention are useful for transforming
5 host cells so as to clone or express the nucleotide sequences of the invention.

Expression can also be achieved using targeted homologous recombination to activate *Chlamydia pneumoniae* genes present in the cloned genomic DNA. A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such that it is operatively linked with an endogenous *Chlamydia pneumoniae* gene present in the cloned genome, using
10 techniques, such as targeted homologous recombination, which are well known to those of skill in the art (See, e.g., Chappel, U.S. Patent No. 4,215,051 and Skoultchi, WO 91/06667 each of which is incorporated herein in its entirety).

Expression vector/host cell systems containing inserts of polynucleotide sequences in SEQ ID No. 1 or ORFs within SEQ ID No. 1, which encode polypeptides, peptides or derivatives, or
15 analogs thereof, can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of a polynucleotide sequence inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted polynucleotide sequence. In the second approach, the recombinant vector/host system can be
20 identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a polynucleotide sequence in the vector. For example, if the polynucleotide sequence in SEQ ID No. 1 or ORFs within SEQ ID No. 1 is inserted within the marker gene sequence of the vector, recombinants containing the insert can be identified by
25 the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the product of the polynucleotide sequence expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of the expressed polypeptide in *in vitro* assay systems, e.g., binding with antibody, promotion of cell proliferation.

Once a particular recombinant DNA molecule is identified and isolated, several methods
30 known in the art may be used to propagate it. The clones identified may be introduced into an appropriate host cell by standard methods, such as for example lipofection, electroporation, and heat shock. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity.

The invention also encompasses the host cells transformed by a vector according to the
35 invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or the expression of the transfected nucleotide sequence.

The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells (Olins and Lee, 1993), but also yeast cells (Buckholz, 1993), as well as animal cells, in particular cultures of mammalian cells (Edwards and Aruffo, 1993), and in particular Chinese hamster ovary (CHO) cells, but also insect cells in which methods using baculoviruses for example
5 may be used (Luckow, 1993).

Furthermore, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host
10 cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation) of proteins. Appropriate cell-lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in
15 mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

A preferred host cell for the expression of the proteins of the invention consists of prokaryotic cells, such as Gram⁺ bacteria. A further preferred host cell according to the invention is a bacterium belonging to the *Chlamydia* family, more preferably belonging to the species *Chlamydia*
20 *pneumoniae* or chosen from a microorganism associated with the species *Chlamydia pneumoniae*.

In other specific embodiments, the polypeptides, peptides or derivatives, or analogs thereof may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences
25 encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer.

Genomic sequences can be cloned and expressed as translational gene products (*i.e.*,
30 peptides, polypeptides, and proteins) or transcriptional gene products (*i.e.*, antisense and ribozymes).

The invention further relates to the intracellular production of an antisense nucleic acid sequence of SEQ ID No. 1 by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would
35 contain a sequence encoding an antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art.

Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the an antisense RNA can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3N long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42), etc.

In a specific embodiment, the antisense oligonucleotide comprises catalytic RNA, or a ribozyme (see, *e.g.*, PCT International Publication WO 90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2N-0-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue *et al.*, 1987, FEBS Lett. 215:327-330).

In another embodiment, the antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a polynucleotide sequence in SEQ ID No. 1. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acid sequence, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA transcribed from SEQ ID No. 1 may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The invention also relates to the animals, except humans, comprising one of the above-described transformed cells according to the invention.

The production of transgenic animals according to the invention overexpressing one or more of the *Chlamydia pneumoniae* genes will be preferably carried out on rats, mice or rabbits according to methods well known to persons skilled in the art such as viral or nonviral transfections. The transgenic animals overexpressing one or more of the said genes may be obtained by transfection of multiple copies of the said genes under the control of a powerful promoter of a ubiquitous nature, or which is selective for one type of tissue. The transgenic animals may also be obtained by homologous recombination on embryonic stem cells, transfer of these stem cells to embryos, selection of the chimeras affected at the level of the reproductive lines, and growth of the said chimeras.

The transformed cells as well as the transgenic animals according to the invention can be used in methods of preparing the recombinant polypeptide.

It is now possible to produce recombinant polypeptides in a relatively large quantity by genetic engineering using the cells transformed with expression vectors according to the invention or using transgenic animals according to the invention.

The methods of preparing a polypeptide of the invention in recombinant form, characterized in that they use a vector and/or a cell transformed with a vector according to the invention and/or a transgenic animal comprising one of the said transformed cells according to the invention, are themselves included in the present invention.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a polypeptide of the cellular envelope of *Chlamydia-pneumoniae* or one of its representative fragments, more preferably encoding a polypeptide of the outer cellular envelope of *Chlamydia pneumoniae* or one of its fragment, are preferred.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide biosynthesis, a Type III or other secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*, are also preferred.

The recombinant polypeptides obtained as indicated above may be provided either in glycosylated or non-glycosylated form and may or may not have the natural tertiary structure.

A preferred variant consists in producing a recombinant polypeptide fused to a "carrier" protein (chimeric protein). The advantage of this system is that it allows a stabilization and a reduction in proteolysis of the recombinant product, an increase in solubility during renaturation in vitro and/or a simplification of purification when the fusion partner has affinity for a specific ligand.

More particularly, the invention relates to a method of preparing a polypeptide of the invention comprising the following steps:

a) culture of the transformed cells under conditions allowing the expression of a recombinant polypeptide having a nucleic acid sequence according to the invention;

b) where appropriate, recovery of the said recombinant polypeptide.

When the method of preparing a polypeptide of the invention uses a transgenic animal according to the invention, the recombinant polypeptide is then extracted from the said animal.

The subject of the invention is also a polypeptide capable of being obtained by a method
5 of the invention as described above.

The invention also comprises a method of preparing a synthetic polypeptide, characterized in that it uses an amino acid sequence of polypeptides according to the invention.

The invention also relates to a synthetic polypeptide obtained by a method according to the invention.

10 Polypeptides according to the invention may also be prepared by conventional techniques in the field of peptide synthesis under conditions suitable to produce the polypeptides encoded by the polynucleotide of the invention. This synthesis may be carried out in and recovered from a homogeneous solution or on a solid phase.

For example, the synthesis technique in a homogeneous solution described by
15 Houbenweyl in 1974 may be used.

This method of synthesis consists in successively condensing, in pairs, the successive amino acids in the required order, or in condensing amino acids and fragments previously formed and already containing several amino acids in the appropriate order, or alternatively several fragments thus previously prepared, it being understood that care will have been taken to protect beforehand all the
20 reactive functional groups carried by these amino acids or fragments, with the exception of the amine functional groups of one and the carboxyl functional groups of the other or vice versa, which should normally take part in the formation of the peptide bonds, in particular after activation of the carboxyl functional group, according to methods well known in peptide synthesis.

According to another preferred technique of the invention, the one described by
25 Merrifield is used.

To manufacture a peptide chain according to the Merrifield method, a highly porous polymer resin is used, onto which the first C-terminal amino acid of the chain is attached. This amino acid is attached onto a resin via its carboxyl group and its amine functional group is protected. The amino acids which will constitute the peptide chain are thus attached, one after another, onto the amine
30 group, each time deprotected beforehand, of the portion of the peptide chain already formed, and which is attached to the resin. When the entire peptide chain desired is formed, the protecting groups are removed from the various amino acids constituting the peptide chain and the peptide is detached from the resin with the aid of an acid.

The invention relates, in addition, to hybrid (fusion) polypeptides having at least one
35 polypeptide or one of its representative fragments according to the invention, and a sequence of a polypeptide capable of eliciting an immune response in humans or animals.

Advantageously, the antigenic determinant is such that it is capable of eliciting a humoral

and/or cellular response. An antigenic determinant may be identified by screening expression libraries of the *Chlamydia pneumoniae* genome with antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*. An antigenic determinant may comprise a polypeptide or one of its representative fragments according to the invention, in glycosylated form, used in order to obtain immunogenic compositions capable of inducing the synthesis of antibodies directed against multiple epitopes. The said polypeptides or their glycosylated fragments also form part of the invention.

These hybrid molecules may consist, in part, of a carrier molecule for polypeptides or for their representative fragments according to the invention, combined with a portion which may be immunogenic, in particular an epitope of the diphtheria toxin, the tetanus toxin, a hepatitis B virus surface antigen (patent FR 79 21811), the poliomyelitis virus VP1 antigen or any other viral or bacterial toxin or antigen.

The methods of synthesizing the hybrid molecules include the methods used in genetic engineering to construct hybrid nucleotide sequences encoding the desired polypeptide sequences. Reference may be advantageously made, for example, to the technique for producing genes encoding fusion proteins described by Minton in 1984.

The said hybrid nucleotide sequences encoding a hybrid polypeptide as well as the hybrid polypeptides according to the invention, characterized in that they are recombinant polypeptides obtained by the expression of the said hybrid nucleotide sequences, also form part of the invention.

The invention also comprises the vectors characterized in that they contain one of the said hybrid nucleotide sequences. The host cells transformed by the said vectors, the transgenic animals comprising one of the said transformed cells as well as the methods of preparing recombinant polypeptides using the said vectors, the said transformed cells and/or the said transgenic animals of course also form part of the invention.

The polypeptides according to the invention, the antibodies according to the invention described below and the nucleotide sequences according to the invention may advantageously be used in *in vitro* and/or *in vivo* methods for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, in a biological sample (biological tissue or fluid) which is likely to contain them. These methods, depending on the specificity of the polypeptides, of the antibodies and of the nucleotide sequences according to the invention which will be used, may in particular detect and/or identify the bacterial variants belonging to the species *Chlamydia pneumoniae* as well as the associated microorganisms capable of being detected by the polypeptides, the antibodies and the nucleotide sequences according to the invention which will be chosen. It may, for example, be advantageous to choose a polypeptide, an antibody or a nucleotide sequence according to the invention, which is capable of detecting any bacterium of the *Chlamydia* family by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the family or, on the contrary, it will be most particularly advantageous to target a variant of the

species *Chlamydia pneumoniae*, which is responsible, for example, for the induction or the worsening of pathologies specific to the targeted variant, by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the said variant.

The polypeptides according to the invention may advantageously be used in a method for
5 the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, in a biological sample (biological tissue or fluid) which is likely to contain them, characterized in that it comprises the following steps:

- a) bringing this biological sample into contact with a polypeptide or one of its representative fragments according to the invention (under conditions allowing an immunological reaction between
10 the said polypeptide and the antibodies which may be present in the biological sample);
- b) detecting the antigen-antibody complexes which may be formed.

Preferably, the biological sample consists of a fluid, for example a human or animal serum, blood or biopsies.

Any conventional procedure may be used to carry out such a detection of the antigen-
15 antibody complexes which may be formed.

By way of example, a preferred method uses immunoenzymatic procedures based on the ELISA technique, immunofluorescence procedures or radioimmunological procedures (RIA), and the like.

Accordingly, the invention also relates to the polypeptides according to the invention,
20 labelled with the aid of a suitable label such as a label of the enzymatic, fluorescent or radioactive type.

Such methods comprise, for example, the following steps:

- deposition of defined quantities of a polypeptide composition according to the invention into the wells of a microtitre plate,
- 25 - introduction, into the said wells, of increasing dilutions of serum, or of a different biological sample as defined above, which has to be analysed,
- incubation of the microplate,
- introduction, into the wells of the microtitre plate, of labelled antibodies directed against human or animal immunoglobulins, these antibodies having been labelled with the aid of an enzyme
30 selected from those which are capable of hydrolyzing a substrate, thereby modifying the absorption of the radiation of the latter, at least at a defined wavelength, for example at 550 nm,
- detection, by comparison with a control, of the quantity of substrate hydrolyzed.

The invention also relates to a kit or set for the detection and/or the identification of
35 bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a polypeptide according to the invention,

- where appropriate, the reagents for constituting the medium appropriate for the immunological or specific reaction,
- the reagents allowing the detection of the antigen-antibody complexes produced by the immunological reaction between the polypeptide(s) of the invention and the antibodies which may be present in the biological sample, it being possible for these reagents also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the polypeptide according to the invention is not labelled,
- where appropriate, a reference biological sample (negative control) free of antibodies recognized by a polypeptide according to the invention,
- 10 - where appropriate, a reference biological sample (positive control) containing a predetermined quantity of antibodies recognized by a polypeptide according to the invention.

According to the invention, the polypeptides, peptides, fusion proteins or other derivatives, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1, may be used as an immunogen to generate antibodies which immunospecifically bind such an immunogen. Such antibodies may include, but are not limited to, polyclonal and monoclonal antibodies, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. In a specific embodiment, the antibody to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1 is a bispecific antibody (see 20 generally, *e.g.* Fanger and Drakeman, 1995, *Drug News and Perspectives* 8: 133-137). Such a bispecific antibody is genetically engineered to recognize both (1) an epitope and (2) one of a variety of "trigger" molecules, *e.g.* Fc receptors on myeloid cells, and CD3 and CD2 on T cells, that have been identified as being able to cause a cytotoxic T-cell to destroy a particular target. Such bispecific antibodies can be prepared either by chemical conjugation, hybridoma, or recombinant molecular 25 biology techniques known to the skilled artisan.

Various procedures known in the art may be used for the production of polyclonal antibodies to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1. For the production of antibody, various host animals can be immunized by injection with a polypeptide, or peptide or other derivative, or analog thereof, including but not limited 30 to rabbits, mice, rats, etc. Various adjuvants, depending on the host species, may be used to increase the immunological response, including but not limited to Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA), Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, 35 surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, BCG (bacille Calmette-Guerin), and corynebacterium parvum. Alternatively, polyclonal antibodies may be prepared by purifying, on an affinity column

onto which a polypeptide according to the invention has been previously attached, the antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*.

For preparation of monoclonal antibodies directed toward a polypeptide, peptide or other
5 derivative, or analog, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983, *Immunology Today* 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, in *Monoclonal*
10 *Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing technology described in PCT/US90/02545. In another embodiment of the invention, transgenic non-human animals can be used for the production of human antibodies utilizing technology described in WO 98/24893 and WO 96/33735. According to the invention, human antibodies may be used and can be obtained by using
15 human hybridomas (Cote *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, *PROC. NATL. ACAD. SCI. U.S.A.* 81:6851-6855; Neuberger *et al.*, 1984, *Nature* 312:604-608; Takeda *et al.*, 1985, *Nature* 314:452-454)
20 by splicing the genes from a mouse antibody molecule specific for a polypeptide, peptide or other derivative, or analog together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

According to the invention, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce polypeptide or peptide-specific single
25 chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.*, 1989, *Science* 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for polypeptides, derivatives, or analogs.

Antibody fragments which contain the idiotype of the molecule can be generated by
30 known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent, and Fv fragments.

In addition, techniques have been developed for the production of chimerized (*See, e.g.*,
35 Boss, M. et al., U.S. Patent No. 4,816,397; and Cabilly, S. et al., U.S. Patent No. 5,585,089 each of which is incorporated herein by reference in its entirety) humanized antibodies (*See, e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) An immunoglobulin

light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of the framework region and CDRs have been precisely defined (See, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983).

- 5 Briefly, humanized antibodies are antibody molecules from non-human species having one or more CDRs from the non-human species and a framework from a human immunoglobulin molecule.

The antibodies of the invention may also be labelled in the same manner as described above for the nucleic probes of the invention such as an enzymatic, fluorescent or radioactive type labelling.

- 10 The invention relates, in addition, to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

- a) bringing the biological sample (biological tissue or fluid) into contact with a mono- or polyclonal antibody according to the invention (under conditions allowing an immunological reaction
15 between the said antibodies and the polypeptides of the bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism which may be present in the biological sample, that is, under conditions suitable for the formation of immune complexes);
- b) detecting the antigen-antibody complex which may be formed.

- 20 Also falling within the scope of the invention is a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a polyclonal or monoclonal antibody according to the invention, labeled where appropriate;
- where appropriate, a reagent for constituting the medium appropriate for carrying out the
25 immunological reaction;
- a reagent allowing the detection of the antigen-antibody complexes produced by the immunological reaction, it being possible for this reagent also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the said monoclonal or polyclonal antibody is not labelled;
- 30 - where appropriate, reagents for carrying out the lysis of the cells in the sample tested.

The principle of the DNA chip which was explained above may also be used to produce protein "chips" on which the support has been coated with a polypeptide or an antibody according to the invention, or arrays thereof, in place of the DNA. These protein "chips" make it possible, for example, to analyze the biomolecular interactions (BIA) induced by the affinity capture of target
35 analytes onto a support coated, for example, with proteins, by surface plasma resonance (SPR). Reference may be made, for example, to the techniques for coupling proteins onto a solid support which are described in EP 524 800 or to the methods describing the use of biosensor-type protein

chips such as the BIAcore-type technique (Pharmacia) (Arlinghaus et al., 1997, Krone et al., 1997, Chatelier et al., 1995). These polypeptides or antibodies according to the invention, capable of specifically binding antibodies or polypeptides derived from the sample to be analysed, may thus be used in protein chips for the detection and/or the identification of proteins in samples. The said protein
5 chips may in particular be used for infectious diagnosis and may preferably contain, per chip, several polypeptides and/or antibodies of the invention of different specificity, and/or polypeptides and/or antibodies capable of recognizing microorganisms different from *Chlamydia pneumoniae*.

Accordingly, the subject of the present invention is also the polypeptides and the antibodies according to the invention, characterized in that they are immobilized on a support, in
10 particular of a protein chip.

The protein chips, characterized in that they contain at least one polypeptide or one antibody according to the invention immobilized on the support of the said chip, also form part of the invention.

The invention comprises, in addition, a protein chip according to the invention,
15 characterized in that it contains, in addition, at least one polypeptide of a microorganism different from *Chlamydia pneumoniae* or at least one antibody directed against a compound of a microorganism different from *Chlamydia pneumoniae*, immobilized on the support of the said chip.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the
20 detection and/or the identification of a microorganism characterized in that it comprises a protein chip according to the invention.

The subject of the present invention is also a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it uses a nucleotide sequence according to
25 the invention.

More particularly, the invention relates to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

- a) where appropriate, isolation of the DNA from the biological sample to be analysed, or optionally
30 production of a cDNA from the RNA in the biological sample;
- b) specific amplification of the DNA of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism with the aid of at least one primer according to the invention;
- c) detection of the amplification products.

35 These may be detected, for example, by the molecular hybridization technique using a nucleic probe according to the invention. This probe will be advantageously labelled with a nonradioactive (cold probe) or radioactive element.

For the purposes of the present invention, "DNA in the biological sample" or "DNA contained in the biological sample" will be understood to mean either the DNA present in the biological sample considered, or optionally the cDNA obtained after the action of a reverse transcriptase-type enzyme on the RNA present in the said biological sample.

5 Another aim of the present invention consists in a method according to the invention, characterized in that it comprises the following steps:

- a) bringing a nucleotide probe according to the invention into contact with a biological sample, the DNA contained in the biological sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to complementary base pairs of the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated-microorganism;
- 10 b) detecting the hybridization complex formed between the nucleotide probe and the DNA in the biological sample.

The present invention also relates to a method according to the invention, characterized in that it comprises the following steps:

- a) bringing a nucleotide probe immobilized on a support according to the invention into contact with a biological sample, the DNA in the sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism;
- 20 b) bringing the hybrid formed between the nucleotide probe immobilized on a support and the DNA contained in the biological sample, where appropriate after removal of the DNA in the biological sample which has not hybridized with the probe, into contact with a labelled nucleotide probe according to the invention;
- 25 c) detecting the new hybrid formed in step b).

According to an advantageous embodiment of the method for the detection and/or the identification defined above, it is characterized in that, prior to step a), the DNA in the biological sample is primer-extended and/or amplified beforehand with the aid of at least one primer according to the invention.

30 The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a) a nucleotide probe according to the invention;
- b) where appropriate, the reagents necessary for carrying out a hybridization reaction;
- 35 c) where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a) a nucleotide probe, called capture probe, according to the invention;
- 5 b) an oligonucleotide probe, called detection probe, according to the invention;
- c) where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of
10 bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a) at least one primer according to the invention;
- b) where appropriate, the reagents necessary for carrying out a DNA amplification reaction;
- c) where appropriate, a component which makes it possible to check the sequence of the amplified
15 fragment, more particularly an oligonucleotide probe according to the invention.

The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the detection and/or the identification of a microorganism characterized in that it comprises a DNA chip according to the invention.

- 20 The invention also relates to a method or to a kit or set according to the invention for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, characterized in that the said primer and/or the said probe according to the invention are chosen from the nucleotide sequences specific to the species *Chlamydia pneumoniae*, in that the said polypeptides according to the invention are chosen from the polypeptides specific to the species *Chlamydia pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides specific to the species *Chlamydia pneumoniae*.

Preferably, the said method or the said kit or set above according to the invention, for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* is
30 characterized in that the said primer and/or the said probe or the said polypeptides are chosen from the nucleotide sequences or polypeptides according to the invention which have been identified as being specific to the species *Chlamydia pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides identified as being specific to the species *Chlamydia pneumoniae*.

- 35 The invention relates, in addition, to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of a condition caused by, cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by a *Chlamydia pneumoniae*

infection.

The invention also relates to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of conditions caused by, respiratory diseases induced or worsened by a *Chlamydia pneumoniae* infection; preferably, the said respiratory disease is asthma.

5 According to another aspect, the subject of the invention is the use of polypeptides according to the invention, of cells transformed with a vector according to the invention and/or of transformed animals according to the invention, for the biosynthesis or the biodegradation of organic or inorganic compounds.

10 As has been mentioned above, the nucleotide sequences of the invention were identified by homology with sequences known to encode, for example, polypeptides or fragments of enzymatic polypeptides involved in the biosynthesis or the biodegradation of organic or inorganic molecules.

It is thus possible to use the said polypeptides of the invention in a similar manner for the biosynthesis or the biodegradation of organic or inorganic compounds of industrial or therapeutic interest (called compounds of interest).

15 Among these polypeptides, there may be mentioned in particular the enzymes involved in metabolism, such as the proteolytic enzymes, amino transferases, glucose metabolism, or the enzymes which may be used in the biosynthesis of sugars, amino acids, fatty acids, polypeptides, nucleotides, nucleic acids or any other organic or inorganic compound or in the biodegradation of organic or inorganic compounds.

20 Among these polypeptides, there may be mentioned, in addition, the mutated or modified enzymes corresponding to mutated or modified polypeptides according to the invention which may also be used for the biosynthesis or the biodegradation of organic or inorganic compounds at the industrial level, such as, for example, the production of compounds of interest, the reprocessing of manufacturing residues applied to the food industries, to the papermaking industry or to the chemical
25 and pharmaceutical industries.

The methods of biosynthesis or biodegradation of organic or inorganic compounds, characterized in that they use a polypeptide or one of its representative fragments according to the invention, transformed cells according to the invention and/or a transformed animal according to the invention, also form part of the invention.

30 The invention relates, in addition, to the use of a nucleotide sequence according to the invention, of a polypeptide according to the invention, of an antibody according to the invention, of a cell according to the invention, and/or of a transformed animal according to the invention, for the selection of an organic or inorganic compound capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the cellular replication of eukaryotic or
35 prokaryotic cells or capable of inducing, inhibiting or worsening the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The invention also comprises screening assays that comprise methods of selecting

compounds capable of binding to a polypeptide, fusion polypeptide or one of its representative fragments according to the invention, capable of binding to a nucleotide sequence according to the invention, or capable of recognizing an antibody according to the invention, and/or capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the growth
5 or the cellular replication of eukaryotic or prokaryotic cells, or capable of inducing, inhibiting or worsening, in an animal or human organism, the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms, characterized in that it comprises the following steps:

a) bringing the said compound into contact with the said polypeptide, the said nucleotide
10 sequence, with a transformed cell according to the invention and/or administering the said compound to a transformed animal according to the invention;

b) determining the capacity of the said compound to bind with the said polypeptide or the said nucleotide sequence, or to modulate, regulate, induce or inhibit the expression of genes, or to modulate growth or cellular replication, or to induce, inhibit or worsen in the said transformed animal,
15 the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The transformed cells and/or animals according to the invention may advantageously serve as a model and may be used in methods for studying, identifying and/or selecting compounds capable of being responsible for pathologies induced or worsened by *Chlamydia pneumoniae*, or
20 capable of preventing and/or of treating these pathologies such as, for example, cardiovascular or respiratory diseases. In particular, the transformed host cells, in particular bacteria of the *Chlamydia* family whose transformation with a vector according to the invention may, for example, increase or inhibit its infectivity, or modulate the pathologies usually induced or worsened by the infection, may be used to infect animals in which the onset of pathologies will be monitored. These nontransformed
25 animals, infected for example with transformed *Chlamydia* bacteria, may serve as a study model. In the same manner, the transformed animals according to the invention may, for example, exhibit predispositions to cardiovascular and/or respiratory diseases and thus be used in methods for selecting compounds capable of preventing and/or of treating the said diseases. The said methods using the said transformed cells and/or transformed animals form part of the invention.

30 The compounds capable of being selected may be organic compounds such as polypeptides or carbohydrates or any other organic or inorganic compounds already known, or new organic compounds produced using molecular modeling techniques and obtained by chemical or biochemical synthesis, these techniques being known to persons skilled in the art.

The said selected compounds may be used to modulate the growth and/or the cellular
35 replication of *Chlamydia pneumoniae* or any other associated microorganism and thus to control infection by these microorganisms. The said compounds according to the invention may also be used to modulate the growth and/or the cellular replication of all eukaryotic or prokaryotic cells, in

particular tumour cells and infectious microorganisms, for which the said compounds will prove active, the methods which make it possible to determine the said modulations being well known to persons skilled in the art.

Compound capable of modulating the growth of a microorganism is understood to
5 designate any compound which makes it possible to act, to modify, to limit and/or to reduce the development, the growth, the rate of proliferation and/or the viability of the said microorganism.

This modulation may be achieved, for example, by an agent capable of binding to a protein and thus of inhibiting or of potentiating its biological activity, or capable of binding to a membrane protein of the outer surface of a microorganism and of blocking the penetration of the said
10 microorganism into the host cell or of promoting the action of the immune system of the infected organism directed against the said microorganism. This modulation may also be achieved by an agent capable of binding to a nucleotide sequence of a DNA or RNA of a microorganism and of blocking, for example, the expression of a polypeptide whose biological or structural activity is necessary for the growth or for the reproduction of the said microorganism.

15 Associated microorganism is understood to designate in the present invention any microorganism whose gene expression may be modulated, regulated, induced or inhibited, or whose growth or cellular replication may also be modulated by a compound of the invention. Associated microorganism is also understood to designate in the present invention any microorganism containing nucleotide sequences or polypeptides according to the invention. These microorganisms may, in some
20 cases, contain polypeptides or nucleotide sequences identical or homologous to those of the invention may also be detected and/or identified by the detection and/or identification methods or kit according to the invention and may also serve as a target for the compounds of the invention.

The invention relates to the compounds capable of being selected by a method of selection according to the invention.

25 The invention also relates to a pharmaceutical composition comprising a compound chosen from the following compounds:

a nucleotide sequence according to the invention;

a polypeptide according to the invention;

a vector according to the invention;

30 an antibody according to the invention; and

a compound capable of being selected by a method of selection according to the invention, optionally in combination with a pharmaceutically acceptable vehicle.

An effective quantity is understood to designate a sufficient quantity of the said compound or antibody, or of a polypeptide of the invention, which makes it possible to modulate the
35 growth of *Chlamydia pneumoniae* or of an associated microorganism.

The invention also relates to a pharmaceutical composition comprising one or more polypeptides according to the invention and/or one or more fusion polypeptides according to the

invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Pharmaceutical compositions include compositions that comprise a polypeptide or fusion polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*. In one embodiment, a pharmaceutical composition according to the invention can be utilized for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention relates, in addition, to an immunogenic composition or a vaccine composition, characterized in that it comprises one or more polypeptides according to the invention and/or one or more hybrid (fusion) polypeptides according to the invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Immunogenic compositions or fusion polypeptide include compositions that comprise a polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

Immunogenic or vaccine compositions can also comprise DNA immunogenic or vaccine compositions comprising polynucleotide sequences of the invention operatively associated with a regulatory sequence that controls gene expression. Such compositions can include compositions that direct expression of a neutralizing epitope of *Chlamydia pneumoniae*.

The invention also comprises the use of a transformed cell according to the invention, for the preparation of a vaccine composition.

The invention also relates to a vaccine composition, characterized in that it contains a nucleotide sequence according to the invention, a vector according to the invention and/or a transformed cell according to the invention.

The invention also relates to the vaccine compositions according to the invention, for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention also relates to the use of DNA encoding polypeptides of *Chlamydia pneumoniae*, in particular antigenic determinants, to be formulated as vaccine compositions. In accordance with this aspect of the invention, the DNA of interest is engineered into an expression vector under the control of regulatory elements, which will promote expression of the DNA, i.e., promoter or enhancer elements. In one preferred embodiment, the promoter element may be cell-specific and permit substantial transcription of the DNA only in predetermined cells. The DNA may be introduced directly into the host either as naked DNA (U.S. Patent No. 5,679,647 incorporated herein by reference in their entirety) or formulated in compositions with other agents which may facilitate uptake of the DNA including viral vectors, i.e., adenovirus vectors, or agents which facilitate immunization, such as bupivacaine and other local anesthetics (U.S. Patent 5,593,972 incorporated herein by reference in their entirety), saponins (U.S. Patent 5,739,118 incorporated herein by reference in their entirety) and cationic polyamines (published international application WO 96/10038 incorporated herein by reference in their entirety).

The DNA sequence encoding the antigenic polypeptide and regulatory element may be inserted into a stable cell line or cloned microorganism, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by
5 reference in its entirety.

Such cell lines and microorganisms may be formulated for vaccine purposes. In yet another embodiment, the DNA sequence encoding the antigenic polypeptide and regulatory element may be delivered to a mammalian host and introduced into the host genome via homologous recombination (*See*, Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is
10 incorporated herein by reference in its entirety.

Preferably, the immunogenic and/or vaccine compositions according to the invention intended for the prevention and/or the treatment of an infection by *Chlamydia pneumoniae* or by an associated microorganism will be chosen from the immunogenic and/or vaccine compositions comprising a polypeptide or one of its representative fragments corresponding to a protein, or one of
15 its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*. The vaccine compositions comprising nucleotide sequences will also preferably comprise nucleotide sequences encoding a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*.

Among these preferred immunogenic and/or vaccine compositions, the most preferred are
20 those comprising a polypeptide or one of its representative fragments, or a nucleotide sequence or one of its representative fragments whose sequences are chosen from the nucleotide or amino acid sequences identified in this functional group and listed above.

The polypeptides of the invention or their representative fragments entering into the immunogenic compositions according to the invention may be selected by techniques known to
25 persons skilled in the art, such as for example on the capacity of the said polypeptides to stimulate T cells, which results, for example, in their proliferation or the secretion of interleukins, and which leads to the production of antibodies directed against the said polypeptides.

In mice, in which a weight dose of the vaccine composition comparable to the dose used in humans is administered, the antibody reaction is tested by collecting serum followed by a study of
30 the formation of a complex between the antibodies present in the serum and the antigen of the vaccine composition, according to the customary techniques.

According to the invention, the said vaccine compositions will be preferably in combination with a pharmaceutically acceptable vehicle and, where appropriate, with one or more appropriate immunity adjuvants.

35 Various types of vaccines are currently available for protecting humans against infectious diseases: attenuated live microorganisms (*M. bovis* - BCG for tuberculosis), inactivated microorganisms (influenza virus), acellular extracts (*Bordetella pertussis* for whooping cough),

recombinant proteins (hepatitis B virus surface antigen), polysaccharides (pneumococci). Experiments are underway on vaccines prepared from synthetic peptides or from genetically modified microorganisms expressing heterologous antigens. Even more recently, recombinant plasmid DNAs carrying genes encoding protective antigens were proposed as an alternative vaccine strategy. This type of vaccination is carried out with a particular plasmid derived from an *E. coli* plasmid which does not replicate *in vivo* and which encodes only the vaccinal protein. Animals were immunized by simply injecting the naked plasmid DNA into the muscle. This technique leads to the expression of the vaccine protein *in situ* and to a cell-type (CTL) and a humoral type (antibody) immune response. This double induction of the immune response is one of the main advantages of the technique of vaccination with naked DNA.

The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization assays such as those described by Peterson et al. (1988) can be utilized. The assay described by Peterson et al. (1988) is suitable for testing vaccine compositions directed toward either *Chlamydia pneumoniae* or *Chlamydia trachomatis*.

Briefly, hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydiae* (10^4 IFU; infectious units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37°C for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37°C for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with a *Chlamydiae* specific antibody, such as anti-MOMP for *C. trachomatis*, etc. IFUs are counted in ten fields at a magnification of 200X. Neutralization titer is assigned based on the dilution that gives 50% inhibition as compared to control monolayers/IFU.

The efficacy of vaccine compositions can be determined *in vivo* by challenging animal models of *Chlamydia pneumoniae* infection, e.g., mice or rabbits, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies can be performed in the murine model of *Chlamydia pneumoniae* infection described by Moazed et al. (1997). Briefly, male homozygous apoE deficient and/or C57 BL/6J mice are immunized with vaccine compositions. Post-vaccination, the mice are mildly sedated by subcutaneous injection of a mixture of ketamine and xylazine, and inoculated intranasally with a total volume of 0.03-0.05 ml of organisms suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately 3×10^7 IFU/mouse. The mice are inoculated with *Chlamydia pneumoniae* at 8, 10, and 12 weeks of age. Tissues are then collected from the lung, spleen, heart, etc. at 1-20 weeks after the first inoculation. The presence of organisms is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

Alternatively, *in vivo* vaccine composition challenge studies can be performed in the rabbit model of *Chlamydia pneumoniae* described by Laitinen et al. (1997). Briefly, New Zealand white rabbits (5 months old) are immunized with the vaccine compositions. Post-vaccination, the rabbits are sedated with Hypnorm, 0.3 ml/Kg of body weight, intramuscularly, and inoculated intranasally with a total of 0.5 ml of *Chlamydia pneumoniae* suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately 3×10^7 IFU/rabbit. The rabbits are reinfected in the same manner and with the same dose 3 weeks after the primary inoculation. Tissues are then collected 2 weeks after the primary infection and 1, 2, and 4 weeks after the reinfection. The presence of *Chlamydia pneumoniae* is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

The vaccine compositions comprising nucleotide sequences or vectors into which the said sequences are inserted are in particular described in International Application No. WO 90/11092 and also in International Application No. WO 95/11307.

The nucleotide sequence constituting the vaccine composition according to the invention may be injected into the host after having been coupled to compounds which promote the penetration of this polynucleotide inside the cell or its transport up to the cell nucleus. The resulting conjugates may be encapsulated into polymeric microparticles, as described in International Application No. WO 94/27238 (Medisorb Technologies International).

According to another embodiment of the vaccine composition according to the invention, the nucleotide sequence, preferably a DNA, is complexed with the DEAE-dextran (Pagano et al., 1967) or with nuclear proteins (Kaneda et al., 1989), with lipids (Felgner et al., 1987) or encapsulated into liposomes (Fraley et al., 1980) or alternatively introduced in the form of a gel facilitating its transfection into the cells (Midoux et al., 1993, Pastore et al., 1994). The polynucleotide or the vector according to the invention may also be in suspension in a buffer solution or may be combined with liposomes.

Advantageously, such a vaccine will be prepared in accordance with the technique described by Tacson et al. or Huygen et al. in 1996 or alternatively in accordance with the technique described by Davis et al. in International Application No. WO 95/11307.

Such a vaccine may also be prepared in the form of a composition containing a vector according to the invention, placed under the control of regulatory elements allowing its expression in humans or animals. It is possible, for example, to use, as vector for the *in vivo* expression of the polypeptide antigen of interest, the plasmid pcDNA3 or the plasmid pcDNA1/neo, both marketed by Invitrogen® & D Systems, Abingdon, United Kingdom). It is also possible to use the plasmid V1Jns.tPA, described by Shiver et al. in 1995. Such a vaccine will advantageously comprise, in addition to the recombinant vector, a saline solution, for example a sodium chloride solution.

The immunogenic compositions of the invention can also be utilized as part of methods for immunization, wherein such methods comprise administering to a host, e.g., a human host, an

immunizing amount of the immunogenic compositions of the invention. In a preferred embodiment, the method of immunizing is a method of immunizing against *Chlamydia pneumoniae*.

A pharmaceutically acceptable vehicle is understood to designate a compound or a combination of compounds entering into a pharmaceutical or vaccine composition which does not
5 cause side effects and which makes it possible, for example, to facilitate the administration of the active compound, to increase its life and/or its efficacy in the body, to increase its solubility in solution or alternatively to enhance its preservation. These pharmaceutically acceptable vehicles are well known and will be adapted by persons skilled in the art according to the nature and the mode of administration of the active compound chosen.

10 As regards the vaccine formulations, these may comprise appropriate immunity adjuvants which are known to persons skilled in the art, such as, for example, aluminum hydroxide, a representative of the family of muramyl peptides such as one of the peptide derivatives of N-acetylmuramyl, a bacterial lysate, or alternatively incomplete Freund's adjuvant, Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI
15 ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA).

Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intranasal, intramuscular, intradermal or subcutaneous route, or by the oral route. More preferably, the vaccine composition comprising polypeptides according to the
20 invention will be administered several times, spread out over time, by the intradermal or subcutaneous route.

Their optimum modes of administration, dosages and galenic forms may be determined according to criteria which are generally taken into account in establishing a treatment adapted to a patient, such as for example the patient's age or body weight, the seriousness of his general condition,
25 tolerance of the treatment and the side effects observed.

The invention comprises the use of a composition according to the invention for the treatment or the prevention of cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by *Chlamydia pneumoniae*.

Finally, the invention comprises the use of a composition according to the invention for
30 the treatment or the prevention of respiratory diseases which are induced or worsened by the presence of *Chlamydia pneumoniae*, preferably asthma.

Other characteristics and advantages of the invention appear in the following examples and figures:

35 Legend to the figures :

Figure 1 : Line for the production of *Chlamydia pneumoniae* sequences

Figure 2 : Analysis of the sequences and assembling

Figure 3 : Finishing techniques

Figure 3a) : Assembly map

Figure 3b) : Determination and use of the orphan ends of the contigs

5

EXAMPLES

Experimental procedures

10

Cells

The *Chlamydia pneumoniae* strain (CM1) used by the inventors is obtained from ATCC (American Culture Type Collection) where it has the reference number ATCC 1360-VR.

It is cultured on HeLa 229 cells, obtained from the American Type Culture Collection,
15 under the reference ATCC CCL-2.1.

Culture of the cells

The HeLa ATCC CCL-2.1 cells are cultured in 75-ml cell culture flasks (Corning). The culture medium is Dulbecco's modified cell culture medium (Gibco BRL No. 04101965) supplemented with MEM amino acids (Gibco BRL - No. 04301140) L (5 ml per 500 ml of medium) and 5% foetal calf serum (Gibco BRL No. 10270 batch 40G8260K) without antibiotics or antifungals.
20

The cell culture stock is maintained in the following manner. The cell cultures are examined under an inverted microscope. 24 hours after confluence, each cellular lawn is washed with PBS (Gibco BRL No. 04114190), rinsed and then placed for 5 min in an oven in the presence of 3 ml of trypsin (Gibco BRL No. 25200056). The cellular lawn is then detached and then resuspended in
25 120 ml of culture medium, the whole is stirred in order to make the cellular suspension homogeneous. 30 ml of this suspension are then distributed per cell culture flask. The flasks are kept in a CO₂ oven (5%) for 48 hours at a temperature of 37°C. The cell stock is maintained so as to have available daily 16 flasks of subconfluent cells. It is these subconfluent cells which will be used so as to be infected with *Chlamydia*. 25-ml cell culture flasks are also used, these flasks are prepared in a similar manner
30 but the volumes used for maintaining the cells are the following: 1 ml of trypsin, 28 ml of culture medium to resuspend the cells, 7 ml of culture medium are used per 25-ml flask.

Infection of the cells with *Chlamydia*

Initially, the *Chlamydiae* are obtained frozen from ATCC (-70°C), in suspension in a volume of 1 ml. This preparation is slowly thawed, 500 µl are collected and brought into contact with
35 subconfluent cells, which are obtained as indicated above, in a 25-ml cell culture flask, containing 1 ml of medium, so as to cover the cells. The flask is then centrifuged at 2000 rpm in a "swing" rotor for microtitre plates, the centrifuge being maintained at a temperature of 35°C. After centrifugation,

the two flasks are placed in an oven at 35°C for three hours. 6 ml of culture medium containing cycloheximide (1 µg/ml) are then added and the flask is stored at 35°C. After 72 hours, the level of infection is evaluated by direct immunofluorescence and by the cytopathogenic effect caused to the cells.

5 Direct immunofluorescence

Starting with infected cells, which were obtained as indicated above, a cellular smear is deposited with a Pasteur pipette on a microscope slide. The cellular smear is fixed with acetone for 10 minutes; after draining the acetone, the smear is covered with 30 µl of murine monoclonal antibodies directed against MOMP (major outer membrane protein) of Chlamydia (Syva, Biomérieux) labelled with fluorescein isothiocyanate. The whole is then incubated in a humid chamber at a temperature of 37°C. The slides are then rinsed with water, slightly dried, and then after depositing a drop of mounting medium, a coverslip is mounted before reading. The reading is carried out with the aid of a fluorescence microscope equipped with the required filters (excitation at 490 nm, emission at 520 nm).

15 Harvesting of the *Chlamydia pneumoniae*

After checking the infection by direct immunofluorescence, carried out as indicated above, the culture flasks are opened under a sterile cabinet, sterile glass beads with a diameter of the order of a millimeter are placed in the flask. The flask is closed and then vigorously stirred while being maintained horizontally, the cellular lawn at the bottom, so that the glass beads can have a mechanical action on the cellular lawn. Most of the cells are thus detached or broken; the effect of the stirring is observed under an optical microscope so as to ensure proper release of Chlamydiae.

20 Large-scale infection of the cell cultures

The product of the Chlamydiae harvest (culture medium and cellular debris) is collected with a pipette, and distributed into three cell culture flasks containing subconfluent HeLa ATCC CCL-2.1 cells, obtained as indicated above. The cells thus inoculated are placed under gentle stirring (swing) in an oven at 35°C. After one hour, the flasks are kept horizontally in an oven so that the culture medium covers the cells for 3 hours. 30 ml of culture medium containing actydione (1 µg/ml) are then added to each of the flasks. The culture flasks are then stored at 35°C for 72 hours. The cells thus infected are examined under an optical microscope after 24 hours, the cytopathogenic effect is evaluated by the appearance of cytoplasmic inclusions which are visible under an inverted optical microscope. After 72 hours, the vacuoles containing the Chlamydiae occupy the cytoplasm of the cell and push the cell nucleus sideways. At this stage, numerous cells are spontaneously destroyed and have left free elementary bodies in the culture medium. The Chlamydiae are harvested as described above and are either frozen at -80°C or used for another propagation.

35 Purification of the Chlamydiae

The product of the Chlamydia harvests is stored at -80°C and thawed on a water bath at

room temperature. After thawing, each tube is vigorously stirred for one minute and immersed for one minute in an ultrasound tank (BRANSON 1200); the tubes are then stirred by inverting before being centrifuged for 5 min at 2000 rpm. The supernatant is carefully removed and kept at cold temperature (ice). The supernatant is vigorously stirred and then filtered on nylon filters having pores
5 of 5 microns in diameter on a support (Nalgene) allowing a delicate vacuum to be established under the nylon filter. For each filtration, three nylon filters are superposed; these filters are replaced after every 40 ml of filtrate. Two hundred milliliters of filtration product are kept at cold temperature, and then after stirring by inverting, are centrifuged at 10,000 rpm for 90 min, the supernatant is removed and the pellet is taken up in 10 ml of 10 mM Tris, vigorously vortexed and then centrifuged at
10 10,000 rpm for 90 min. The supernatant is removed and the pellet is taken up in a buffer (20 mM Tris pH 8.0, 50 mM KCl, 5 mM MgCl₂) to which 800 units of DNase I (Boehringer) are added. The whole is kept at 37°C for one hour. One ml of 0.5 M EDTA is then added, the whole is vortexed and frozen at -20°C.

Preparation of the DNA

15 The Chlamydiae purified above are thawed and subjected to a proteinase K (Boehringer) digestion in a final volume of 10 ml. The digestion conditions are the following: 0.1 mg/ml proteinase K, 0.1 × SDS at 55EC, stirring every 10 min. The product of digestion is then subjected to a double extraction with phenol-chloroform, two volumes of ethanol are added and the DNA is directly recovered with a Pasteur pipette having one end in the form of a hook. The DNA is dried on the edge
20 of the tube and then resuspended in 500 µl of 2 mM Tris pH 7.5. The DNA is stored at 4°C for at least 24 hours before being used for the cloning.

Cloning of the DNA

After precipitation, the DNA is quantified by measuring the optical density at 260 nm. Thirty µg of Chlamydia DNA are distributed into 10 tubes of 1.5 ml and diluted in 300 µl of water.
25 Each of the tubes is subjected to 10 applications of ultrasound lasting for 0.5 sec in a sonicator (unisonix XL2020). The contents of the 10 tubes are then grouped and concentrated by successive extractions with butanol (Sigma B1888) in the following manner: two volumes of butanol are added to the dilute DNA mixture. After stirring, the whole is centrifuged for five minutes at 2500 rpm and the butanol is removed. This operation is repeated until the volume of the aqueous phase is less than 1 ml.
30 The DNA is then precipitated in the presence of ethanol and of 0.5 M sodium acetate pH 5.4, and then centrifuged for thirty minutes at 15,000 rpm at cold temperature (4°C). The pellet is washed with 75% ethanol, centrifuged for five minutes at 15,000 rpm and dried at room temperature. A tenth of the preparation is analysed on a 0.8% agarose gel. Typically, the size of the DNA fragments thus prepared is between 200 and 8000 base pairs.

35 To allow the cloning of the DNA obtained, the ends are repaired. The DNA is distributed in an amount of 10 µg/tube, in the following reaction medium: 100 µl final volume, 1 × buffer

(Biolabs 201L), 0.5 µl BSA 0.05 mg/ml, 0.1 mM dATP, 0.1 mM each of dGTP, dCTP or dTTP, 60,000 IU T4 DNA polymerase. The reaction is incubated for thirty minutes at 16°C. The contents of each of the tubes are then grouped before carrying out an extraction with phenol-chloroform and then precipitating the aqueous phase as described above. After this step, the DNA thus prepared is phosphorylated. For that, the DNA is distributed into tubes in an amount of 10 µg per tube, and then in a final volume of 50 µl, the reaction is prepared in the following manner: 1 mM ATP, 1 × kinase buffer, 10 IU T4 polynucleotide kinase (Biolabs 201L). The preparation is incubated for thirty minutes at 37°C. The contents of the tubes are combined and a phenol-chloroform extraction and then a precipitation are carried out in order to precipitate the DNA. The latter is then suspended in 1 µl of water and then the DNA fragments are separated according to their size on a 0.8% agarose gel (1 × TAE). The DNA is subjected to an electric field of 5 V/cm and then visualized on a UV table. The fragments whose size varies between 1200 and 2000-base pairs are selected by cutting out the gel. The gel fragment thus isolated is placed in a tube and then the DNA is purified with the Qiaex kit (20021 Qiagen), according to the procedure provided by the manufacturer.

15 Preparation of the vector

14 µg of the cloning vector pGEM-5Zf (Proméga P2241) are diluted in a final volume of 150 µl and are subjected to digestion with the restriction enzyme EcoRV 300 IU (Biolabs 195S) according to the protocol and with the reagents provided by the manufacturer. The whole is placed at 37°C for 150 min and then distributed in the wells of a 0.8% agarose gel subjected to an electric field of 5 V/cm. The linearized vector is visualized on a UV table, isolated by cutting out the gel and then purified by the Qiaex kit (Qiagen 20021) according to the manufacturer's recommendations. The purification products are grouped in a tube, the volume is measured and then half the volume of phenol is added and the whole is vigorously stirred for 1 min. Half the volume of chloroform-isoamyl alcohol 24:1 is added and vigorously stirred for 1 min. The whole is centrifuged at 15,000 rpm for 5 min at 4°C, the aqueous phase is recovered and transferred into a tube. The DNA is precipitated in the presence of 0.3 M sodium acetate, pH 5.4 and 3 volumes of ethanol and placed at -20°C for 1 hour. The DNA is then centrifuged at 15,000 rpm for 30 min at 4°C, the supernatant is removed while preserving the pellet, washed twice with 70% ethanol. After drying at room temperature, the DNA is suspended in 25 µl of water.

30 Phosphorylation of the vector

25 µl of the vector prepared in the preceding step are diluted in a final volume of 500 µl of the following reaction mixture:

After repair, the DNA is subjected to a phenol-chloroform extraction and a precipitation, the pellet is then taken up in 10 µl of water, the DNA is quantified by measuring the optical density at 260 nm. The quantified DNA is ligated into the vector pGEM-5Zf(+) prepared by the restriction

enzyme EcoRV and dephosphorylated (see preparation of the vector). The ligation is carried out under three conditions which vary in the ratio between the number of vector molecules and the number of insert molecules. Typically, an equimolar ratio, a ratio of 1:3 and a ratio of 3:1 are used for the ligations which are, moreover, carried out under the following conditions: vector PGEm-5Zf(+)

5 25 ng, cut DNA, ligation buffer in a final volume of 20 µl with T4 DNA ligase (Amersham E70042X); the whole is then placed in a refrigerator overnight and then a phenol-chloroform extraction and a precipitation are carried out in a conventional manner. The pellet is taken up in 5 µl of water.

Transformation of the bacteria

Plating of the bacteria

10 Petri dishes containing LB Agar medium containing ampicillin (50 µg/ml), Xgal (280 µg/ml) [5-bromo-4-chloro-indolyl-beta-D-galactopyranoside (Sigma B-4252)], IPTG (140 µg/ml) [isopropyl-beta-D-thiogalactoside (Sigma I-6758)] are used, 50 and 100 µl of bacteria are plated for each of the ligations. The Petri dishes are placed upside down at 37°C for 15 to 16 hours in an oven. The number of "recombinant" positive clones is evaluated by counting the white colonies and

15 the blue colonies which are thought to contain the vector alone.

Evaluation of the "recombinant" positive clones

Ninety-four white colonies and two blue colonies are collected with the aid of sterile cones and are deposited at the bottom of the wells of plates designed for carrying out the amplification techniques. 30 µl of the following reaction mixture are added to each well: 1.7 mM MgCl₂, 0.2 mM

20 each of dATP, dCTP, dGTP and dTTP, two synthetic oligonucleotides corresponding to sequences flanking the cloning site on either side and orienting the synthesis of the DNA in a convergent manner (0.5 µM RP and PU primers, 1 U TAQ polymerase (GibcoBRL 18038-026)).

The colonies thus prepared are subjected to a temperature of 94°C for 5 min and then to 30 thermal cycles composed of the following steps: 94°C for 40 s, 50°C for 30 s, 72°C for 180 s. The

25 reaction is then kept for 7 min at 72°C and then kept at 4°C.

The amplification products are deposited on an agarose gel (0.8%), stained with ethidium bromide, subjected to electrophoresis, and then analysed on an ultraviolet table. The presence of an amplification fragment having a size greater than 500 base pairs indicates the presence of an insert. The bacterial clones are then prepared so as to study the sequence of their insert.

Sequencing

To sequence the inserts of the clones obtained as above, these were amplified by PCR on bacteria cultures carried out overnight using the primers for the vectors flanking the inserts. The sequence of the ends of these inserts (on average 500 bases on each side) was determined by automated fluorescent sequencing on an ABI 377 sequencer, equipped with the ABI Prism DNA

35 Sequencing Analysis software (version 2.1.2).

Analysis of the sequences

The sequences obtained by sequencing in a high-yield line (Figure 1) are stored in a database; this part of the production is independent of any treatment of the sequences. The sequences are extracted from the database, avoiding all the regions of inadequate quality, that is to say the regions for which uncertainties are observed on the sequence at more than 95%. After extraction, the sequences are introduced into a processing line, the diagram of which is described in Figure 2. In a first path of this processing line, the sequences are assembled by the Gap4 software from R. Staden (Bonfield et al., 1995) (OS UNIX/SUN Solaris); the results obtained by this software are kept in the form of two files which will be used for a subsequent processing. The first of these files provides information on the sequence of each of the contigs obtained. The second file represents all the clones participating in the composition of all the contigs as well as their positions on the respective contigs.

The second processing path uses a sequence assembler (TIGR-Asmg assembler UNIX/SUN Solaris); the results of this second processing path are kept in the form of a file in the TIGR-Asmg format which provides information on the relationship existing between the sequences selected for the assembly. This assembler is sometimes incapable of linking contigs whose ends overlap over several hundreds of base pairs.

The results obtained from these two assemblers are compared with the aid of the BLAST program, each of the contigs derived from one assembly path being compared with the contigs derived from the other path.

For the two processing paths, the strict assembly parameters are fixed (95% homology, 30 superposition nucleotides). These parameters avoid 3 to 5% of the clones derived from eukaryotic cells being confused with sequences obtained from the clones derived from *Chlamydia pneumoniae*. The eukaryotic sequences are however preserved during the course of this project; the strategy introduced, which is described below, will be designed, inter alia, not to be impeded by these sequences derived from contaminating clones.

The results of these two assemblers are processed in a software developed for this project. This software operates on a Windows NT platform and receives, as data, the results derived from the STADEN software and/or the results derived from the TIGR-Asmg assembler, the software, results, after processing of the data, in the determination of an assembly map which gives the proximity relationship and the orientation of the contigs in relation to one another (Figure 3a). Using this assembly map, the software determines all the primers necessary for finishing the project. This treatment, which will be detailed below, has the advantage of distinguishing the isolated sequences derived from the contaminations, by the DNA eukaryotic cells, of the small-sized sequences clearly integrated into the project by the relationships which they establish with contigs. In order to allow, without any risk of error, the arrangement and the orientation of the contigs in relation to one another, a statistical evaluation of the accuracy of the names (naming) "naming" of sequence is made from the results of "contigation". This evaluation makes it possible to give each of the clone plates, as well as each of the subsets of plates, a weight which is inversely proportional to probable error rate existing in

the "naming" of the sequences obtained from this plate or from a subset of this plate. In spite of a low error rate, errors may occur throughout the steps of production of the clones and of the sequences. These steps are numerous, repetitive and although most of them are automated, others, like the deposition in the sequencers, are manual; it is then possible for the operator to make mistakes such as the inversion of two sequences. This type of error has a repercussion on the subsequent processing of the data, by resulting in relationships (between the contigs) which do not exist in reality, then in attempts at directed sequencing between the contigs which will end in failure. It is because of this that the evaluation of the naming errors is of particular importance since it allows the establishment of a probabilistic assembly map from which it becomes possible to determine all the clones which will serve as template to obtain sequences separating two adjacent contigs. Table 2 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the clones and the sequences of the primers initially used during the initial operations.

To avoid the step which consists in ordering and then preparing the clones by conventional microbiological means, outer and inner primers oriented towards the regions not yet sequenced are defined by the software. The primers thus determined make it possible to prepare, by PCR, a template covering the nonsequenced region. It is the so-called outer primers (the ones most distant from the region to be sequenced) which are used to prepare this template. The template is then purified and a sequence is obtained on each of the two strands during 2 sequencing reactions which each use one of the 2 inner primers. In order to facilitate the use of this approach, the two outer primers and the two inner primers are prepared and then stored on the same position of 4 different 96-well plates. The two plates containing the outer primers are used to perform the PCRs which will serve to prepare the templates. These templates will be purified on purification columns preserving the topography of the plates. Each of the sequences will be obtained using primers situated on one and then on the other of the plates containing the inner primers. This distribution allows a very extensive automation of the process and results in a method which is simple to use for finishing the regions not yet sequenced. Table 3 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the names and the sequences of the primers used for finishing *Chlamydia pneumoniae*.

Finally, a number of contigs exist in a configuration where one of their ends is not linked to any other contig end (Figure 3b) by a connecting clone relationship (a connecting clone is defined as a clone having one sequence end on a contig and the other end of its sequence on another contig; furthermore, this clone must be derived from a plate or a subset of plates with adequate naming quality). For the *Chlamydia pneumoniae* project, this particular case occurred 24 times. Two adjacent PCR primers orienting the synthesis of the DNA towards the end of the consensus sequence are defined for each of the orphan ends of the consensus sequence. The primer which is closest to the end

of the sequence is called the inner primer whereas the primer which is more distant from the end of the sequence is called the outer primer. The outer primers are used to explore the mutual relationship between the orphan ends of the different contigs. The presence of a single PCR product and the possibility of amplifying this product unambiguously using the inner primers evokes the probable relationship between the contigs on which the primers which allowed the amplification are situated. This relationship will be confirmed by sequencing and will allow the connection between the orphan ends of the consensus sequences. This strategy has made it possible to obtain a complete map of the *Chlamydia pneumoniae* chromosome and then to finish the project.

Quality control

All the bases not determined with certainty in the chromosomal sequence were noted and the density of uncertainties was measured on the entire chromosome. The regions with a high density of uncertainties were noted and the PCR primers spanning these regions were drawn and are represented in Table 4 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997 each of which is incorporated by reference herein in its entirety.

The sequence of each of the PCR products was obtained with two operational primers different from the amplification primers. The sequences were obtained in both directions for all the PCRs (100% success).

Data banks

Local reorganizations of major public banks were used. The protein bank used consists of the nonredundant fusion of the Genpept bank (automated translation of GenBank, NCBI; Benson et al., 1996).

The entire BLAST software (public domain, Altschul et al., 1990) for searching for homologies between a sequence and protein or nucleic data banks was used. The significance levels used depend on the length and the complexity of the region tested as well as the size of the reference bank. They were adjusted and adapted to each analysis.

The results of the search for homologies between a sequence according to the invention and protein or nucleic data banks are presented and summarized in Table 1 below.

Table 1: List of coding chromosome regions and homologies between these regions and the sequence banks.

Legend to Table 1: Open reading frames are identified with the GenMark software version 2.3A (GenePro), the template used is *Chlamydia pneumoniae* of order 4 on a length of 196 nucleotides with a window of 12 nucleotides and a minimum signal of 0.5. The reading frames ORF2 to ORF 1137 are numbered in order of appearance on the chromosome, starting with ORF2 (ORF column). The positions of the beginning and of the end are then given in column 2 (position). When the position of the beginning is greater than the position of the end, this means that the region is

encoded by the strand complementary to the sequence which was given in the sequence SEQ ID No. 1.

All the putative products were subjected to a search for homology on GENPEPT (release 102 for SEQ ID No. 2 to SEQ ID No. 1137, and release 108 for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849) with the BLASTP software (Altschul et al. 1990). With, as parameters, the default parameters with the exception of the expected value E set at 10^{-5} (for SEQ ID No. 2 to SEQ ID No. 1137) and P value set at e^{-10} (for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849). Subsequently, only the identities greater than 30% (1% column) were taken into account. The description of the most homologous sequence is given in the Homology column; the identifier for the latter sequence is given in the ID column and the animal species to which this sequence belongs is given in the Species column. The Homology score is evaluated by the sum of the blast scores for each region of homology and reported in the Score column.

Materials and Methods for transmembrane domains:

The DAS software was used as recommended by the authors (Cserzo et al., 1997).

This method uses, to predict the transmembrane domains, templates derived from a sampling of selected proteins. All the regions for which a "Cutoff" greater than 1.5 was found by the program were taken into account.

Additional ORF Finder Programs

For this analysis, two additional ORF finder programs were used to predict potential open reading frames of a minimum length of 74 amino acids; Glimmer (Salzberg, S.L., Delcher, A., Kasif, S., and W. White. 1998. Microbial gene identification using interpolated Markov models. Nucleic Acids Res. 26:544-548.), and an in-house written program. The in-house program used a very simple search algorithm. The analysis required the that the genomic DNA sequence text be in the 5' to 3' direction, the genome is circular, and that TAA, TAG, and TGA are stop codons. The search parameters were as follows:

- (1) A search for an ORF that started with a GTG codon was performed. If no GTG codons were found, then a search for an ATG codon was performed. However, if a GTG codon was found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.
- (2) A search for an ORF that started with a TTG codon was performed. If no TTG codons were found, then a search for a ATG codon was performed. However, if a TTG codon was found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.
- (3) The analysis described in steps 1 and 2 were repeated for the opposite strand of DNA sequence.

- (4) A search for ORFs that determined all ORF lengths using start and stop positions in the same reading frames was performed.
- (5) All ORFs whose DNA length was less than 225 nucleotides were eliminated from the search.

5 Surface Exposed Protein Search Criteria

Potential cell surface vaccine targets are outer membrane proteins such as porins, lipoproteins, adhesions and other non-integral proteins. In *Chlamydia psittaci*, the major immunogens is a group of putative outer membrane proteins (POMPs) and no homologs have been found in *Chlamydia pneumoniae* and *Chlamydia trachomatis* by traditional analysis (Longbottom, D., Russell,
10 M., Dunbar, S.M., Jones, G.E., and A.J. Herring. 1998. Molecular Cloning and Characterization of the Genes Coding for the Highly Immunogenic Cluster of 90-Kilodalton Envelope Proteins from *Chlamydia psittaci* Subtype That Causes Abortion in Sheep. Infect Immun 66:1317-1324.) Several putative outer membrane proteins have been identified in *Chlamydia pneumoniae*, all of which may represent vaccine candidates. The major outer membrane protein (MOMP) gene (omp1) has been
15 found in various isolates of *Chlamydia pneumoniae* (Jantos, CA., Heck, S., Roggendorf, R., Sen-Gupta, M., and Hegemann, JH. 1997. Antigenic and molecular analyses of different chlamydia pneumoniae strains. J. Clin Microbiology 35(3):620-623.) Various criteria, as listed below, were used to identify putative surface exposed ORFs from the genomic DNA sequence of *Chlamydia pneumoniae* (French application 97-14673 filed 21 November 1997). Any ORF which met any one or
20 more of the individual criteria were listed in this category.

Protein homology searches were done using the Blastp 2.0 tool (Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., and D.J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402.) An ORF product was labeled surface exposed if there was homology to a known, or
25 hypothetical, or putative surface exposed protein with a P score better than e^{-10} .

Most, if not all, proteins that are localized to the membrane of bacteria, via a secretory pathway, contain a signal peptide. A software program, SignalP, analyzes the amino acid sequence of an ORF for such a signal peptide (Nielsen, H., Engelbrecht, J., Brunak, S., and G. von Heijne. 1997. Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites.
30 Protein Engineering 10:1-6.) The first 60 N-terminal amino acids of each ORF were analyzed by SignalP using the Gram-Negative software database. The output generates four separate values, maximum C, maximum Y, maximum S, and mean S. The S-score, or signal region, is the probability of the position belonging to the signal peptide. The C-score, or cleavage site, is the probability of the position being the first in the mature protein. The Y-score is the geometric average of the C-score and
35 a smoothed derivative of the S-score. A conclusion of either a Yes or No is given next to each score. If all four conclusions are Yes and the C-terminal amino acid is either a phenylalanine (F) or a tyrosine (Y), the ORF product was labelled outer membrane (Struyve, M., Moons, M., and J. Tommassen.

1991. Carboxy-terminal Phenylalanine is Essential for the Correct Assembly of a Bacterial Outer Membrane Protein. J. Mol. Biol. 218:141-148.)

The program called Psort, determines the localization of a protein based on its signal sequence, recognition of transmembrane segments, and analysis of its amino acid composition (Nakai, 5 K., and M. Kanehisa. 1991. Expert system for predicting protein localization sites in gram-negative bacteria. Proteins 11:95-110.) An ORF product is considered to be an outer membrane protein if the output data predicts the protein as outer membrane with a certainty value of 0.5 or better and whose value is at least twice as large as the next predicted localized certainty value.

Finally, ORF products that were not predicted to be outer membrane or surface exposed, 10 based on the above criteria, were further analyzed. The blastp output data for these ORFs were searched using various general and specific keywords, suggestive of known cell surface exposed proteins. An ORF was labeled surface exposed if the keywords matched had a Blastp hit, had a P score better than e^{-10} , and that there was no better data indicating otherwise. The following is a list of the searched keywords:

15

	Adhesion	Adhesin	Invasin	Invasion	Extensin	
	Omp	Outer Surface	Porin	Outer Membrane		
	Cell Surface	Cell Wall	Pilus	Pilin	Flagellar sheath	BtuB
	Cir	ChuA	CopB	ExeD	FadL	FecA
20	FepA	FhuA	FmdC	FomA	FrpB	GspD
	HemR	HgbA	Hgp	HmbR	HmuR	HMW
	HrcC	Hrp	InvG	LamB	LbpA	LcrQ
	Lmp1	MxiD	MOMP	PilE	HpaA	NoIW
	NspA	OpcP	OpnP	Opr	OspA	PhoE
25	PldA	Por	PscC	PulD	PupA	QuiX
	RafY	ScrY	SepC	ShuA	SomA	SpiA
	Tbp1	Yop	YscC	mip	Tol	

Those ORFs that did not meet the minimum requirement for being an outer membrane protein based 30 on the above search criteria but which were homologous to identified outer membrane ORFs in *Chlamydia trachomatis* were included. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of outer membrane ORFs were identified. These *Chlamydia trachomatis* ORFs were then tested against the *Chlamydia pneumoniae* genome 35 using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value better than e^{-10} against a *Chlamydia trachomatis* outer membrane was included in this section, if there was no better data

indicating otherwise. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative surface exposed proteins is set forth above in the specification.

Identification of Putative Lipoproteins in the Genome of *Chlamydia pneumoniae*

5 Lipoproteins are the most abundant post-translationally modified bacterial secretory proteins (Pugsley, A. P., 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The characteristic features of lipoproteins are a thiol-linked diacylglyceride and an amine-linked monoacyl group on the cysteine that becomes the amino-terminal residue after signal peptide cleavage by Signal Peptidase II.
10 (Pugsley, A. P., 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The identification of putative lipoproteins from the genomic sequencing of *Chlamydia pneumoniae* was done by examining the deduced amino acid sequence of identified ORFs for the presence of a signal peptide with a Signal Peptidase II cleavage site analogous to the consensus sequence for prolipoprotein modification and
15 processing reactions (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. In N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.).

20 *Chlamydia pneumoniae* ORFs were initially screened for the most basic of lipoprotein characteristics, a cysteine in the first 30 amino acids of the deduced protein. ORFs with a standard start codon (ATG, GTG, or TTG) and having one or more of the following characteristics were selected for direct analysis of their first 30 amino acids:

(a) Significant Signal P value (at least two out of the four values are Yes)

25

(b) PSORT value indicating membrane passage (IM-inner membrane, Peri-periplasm, or OM-outer membrane)

(c) Identification of the word lipoprotein among the ORF blastp data set.

30 (d) A Blastp value of $<e^{-10}$ with a putative lipoprotein from *Chlamydia trachomatis* (French applications 97-15041 filed 28 November 1997 and 97-16034 filed 17 December 1997).

The first 30 amino acids of each ORF in this set were analyzed for the characteristics commonly found in lipoprotein signal peptides (Pugsley, A. P., 1993. The complete general secretory
35 pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108; Hayashi, S., and H. C. Wu. 1992.

Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. In N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.) Putative lipoprotein signal peptides were required to have a
 5 cysteine between amino acid 10 and 30 and reach a minimum score of three based on the following criteria for lipoprotein signal peptides:

- (a) Identification of specific amino acids in specific positions around the cysteine which are part of the consensus Signal Peptidase II cleavage site (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. In N. M.
 10 Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York); Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128). Since the identification of the cleavage site is the most important factor in identifying putative lipoproteins, each correctly positioned amino acid contributed toward reaching the minimum score of three.
- (b) A hydrophobic region rich in alanine and leucine prior to the cleavage site (Pugsley, A. P.. 1993. The
 15 complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.
- (c) A short stretch of hydrophilic amino acids greater than or equal to 1 usually lysine or arginine following the N-terminal methionine (Pugsley, A. P.. 1993. The complete
 20 general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.

A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative lipoproteins is set forth above in the specification.

25 LPS-Related ORFs of *Chlamydia pneumoniae*

Lipopolysaccharide (LPS) is an important major surface antigen of *Chlamydia* cells. Monoclonal antibodies (Mab) directed against LPS of *Chlamydia pneumoniae* have been identified that can neutralize the infectivity of *Chlamydia pneumoniae* both in vitro and in vivo (Peterson, E.M., de la Maza, L.M., Brade, L., Brade, H. 1998. Characterization of a Neutralizing Monoclonal
 30 Antibody Directed at the Lipopolysaccharide of *Chlamydia pneumoniae*. Infect. Immun. Aug. 66(8):3848-3855.) Chlamydial LPS is composed of lipid A and a core oligosaccharide portion and is phenotypically of the rough type (R-LPS) (Lukacova, M., Baumann, M., Brade, L., Mamat, U., Brade, H. 1994. Lipopolysaccharide Smooth-Rough Phase Variation in Bacteria of the Genus *Chlamydia*. Infect. Immun. June 62(6):2270-2276.) The lipid A component is composed of fatty acids
 35 which serve to anchor LPS in the outer membrane. The core component contains sugars and sugar derivatives such as a trisaccharide of 3-deoxy-D-manno-octulosonic acid (KDO) (Reeves, P.R., Hobbs, M., Valvano, M.A., Skurnik, M., Whitfield, C., Coplin, D., Kido, N., Klena, J., Maskell, D.,

Raetz, C.R.H., Rick, P.D. 1996. *Bacterial Polysaccharide Synthesis and Gene Nomenclature* pp. 10071-10078, Elsevier Science Ltd.). The KDO gene product is a multifunctional glycosyltransferase and represents a shared epitope among the Chlamydia. For a review of LPS biosynthesis see, e.g., Schnaitman, C.A., Klena, J.D. 1993. Genetics of Lipopolysaccharide
 5 Biosynthesis in Enteric Bacteria. Microbiol. Rev. 57:655-682.

A text search of the ORF blastp results identified several genes that are involved in Chlamydial LPS production with a P score better than e^{-10} . The following key-terms were used in the text search: KDO, CPS (Capsular Polysaccharide Biosynthesis), capsule, LPS, rfa, rfb, rfc, rfe, rha, rhl, core, epimerase, isomerase, transferase, pyrophosphorylase, phosphatase, aldolase, heptose,
 10 manno, glucose, lpxB, fibronectin, fibrinogen, fucosyltransferase, lic, lgt, pgm, tolC, rol, ChoP, phosphorylcholine, waaF, PGL-Tb1. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative polypeptides involved in LPS biosynthesis is set forth above in the specification.

Type III And Other Secreted Products

15 Type III secretion enables gram-negative bacteria to secrete and inject pathogenicity proteins into the cytosol of eukaryotic host cells (Hueck, C. J., 1998. Type III Protein Secretion Systems in Bacterial Pathogens of Animals and Plants. In Microbiology and Molecular Biology Reviews. 62:379-433.) These secreted factors often resemble eukaryotic signal transduction factors, thus enabling the bacterium to redirect host cell functions (Lee, C.A., 1997. Type III secretion
 20 systems: machines to deliver bacterial proteins into eukaryotic cells? Trends Microbiol. 5:148-156.) In an attempt to corrupt normal cellular functions, Chlamydial pathogenicity factors injected into the host cytosol will nonetheless, as cytoplasmic constituents be processed and presented in the context of the Major Histocompatibility Complex (MHC class I). As such, these pathogenicity proteins represent MHC class I antigens and will play an important role in cellular immunity. Also included in this set
 25 are secreted non-type III products that may play a role as vaccine components.

A text search of the ORF blastp results identified genes that are involved in *Chlamydia pneumoniae* protein secretion with a P score better than e^{-10} . The following key-terms were used in the text search in an effort to identify surface localized or secreted products: Yop, Lcr, Ypk, Exo, Pcr, Pop, Ipa, Vir, Ssp, Spt, Esp, Tir, Hrp, Mxi, hemolysin, toxin, IgA protease, cytolysin, tox, hap,
 30 secreted and Mip.

Chlamydia pneumoniae ORFs that did not meet the above keyword search criteria, but have homologs in *Chlamydia trachomatis* that do meet the search criteria are included herein. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of
 35 ORFs were identified. These *Chlamydia trachomatis* ORFs were tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value $< e^{-10}$ against a *Chlamydia trachomatis* homolog, identified using the above search criteria, was included. A

list of ORFs in the *Chlamydia pneumoniae* genome encoding putative secreted proteins is in the specification.

Chlamydia pneumoniae: RGD Recognition Sequence

5 Proteins that contain Arg-Gly-Asp (RGD) attachment site, together with integrins that serve as their receptor constitute a major recognition system for cell adhesion. The RGD sequence is the cell attachment site of a large number of adhesive extracellular matrix, blood, and cell surface proteins and nearly half of the known integrins recognize this sequence in their adhesion protein ligands. There are many RGD containing microbial proteins such as the penton protein of adenovirus,
10 the coxsackie virus, the foot and mouth virus and pertactin, a 69 kDa (kilodalton) surface protein of *Bordetella pertussis*, that serve as ligands through which these microbes bind to integrins on the cell surfaces and gain entry into the cell. The following provides evidence supporting the importance of RGD in microbial adhesion:

a) The adenovirus penton base protein has a cell rounding activity and when penton base was
15 expressed in *E. coli*, it caused cell rounding and cells adhered to polystyrene wells coated with the protein. Mutant analysis showed that both these properties required an RGD sequence. Virus mutants with amino acid substitutions in the RGD sequence, showed much less adherence to HeLa S3 cells, and also were delayed in virus reproduction (Bai, M., Harfe, B., and Freimuth, P. 1993. Mutations That Alter an RGD Sequence in the Adenovirus Type 2
20 Penton Base Protein Abolish Its Cell-Rounding Activity and Delay Virus Reproduction in Flat Cells. *J. Virol.* 67:5198-5205).

b) It has been shown that attachment and entry of coxsackie virus A9 to GMK cells were dependent on an RGD motif in the capsid protein VP1. VP1 has also been shown to bind $\alpha_v\beta_3$
25 integrin, which is a vitronectin receptor (Roivainen, M., Piirainen, L., Hovi, T., Virtanen, I., Riikonen, T., Heino, J., and Hyypia, T. 1994. Entry of Coxsackievirus A9 into Host Cells: Specific Interactions with $\alpha_v\beta_3$ Integrin, the Vitronectin Receptor *Virology*, 203:357-65).

c) During the course of whooping cough, *Bordetella pertussis* interacts with alveolar
30 macrophages and other leukocytes on the respiratory epithelium. Whole bacteria adheres by means of two proteins, filamentous hemagglutinin (FHA) and pertussis toxin. FHA interacts with two classes of molecules on macrophages, galactose containing glycoconjugates and the integrin CR3. The interaction between CR3 and FHA involves recognition of RGD sequence at the positions 1097-1099 in FHA (Relman, D., Tuomanen, E., Falkow, S., Golenbock, D. T.,
35 Saukkonen, K., and Wright, S. D. "Recognition of a Bacterial Adhesin by an Integrin: Macrophage CR3 Binds Filamentous Hemagglutinin of *Bordetella Pertussis*." *Cell*, 61:1375-1382 (1990)).

- d) Pertactin, a 69 kDa outer membrane protein of *Bordetella pertussis*, has been shown to promote attachment of Chinese hamster ovary cells (CHO). This attachment is mediated by recognition of RGD sequence in pertactin by integrins on CHO cells and can be inhibited by synthetic RGD containing peptide homologous to the one present in pertactin (Leininger, E., Roberts, M., Kenimer, J. G., Charles, I. G., Fairweather, N., Novotny, P., and Brennan, M. J. 1991. Pertactin, an Arg-Gly-Asp containing *Bordetella pertussis* surface protein that promotes adherence of mammalian cells Proc. Natl. Acad. Sci. USA, 88:345-349).
- 5
- e) The RGD sequence is highly conserved in the VP1 protein of foot and mouth disease virus (FMDV). Attachment of FMDV to baby hamster kidney cells (BHK) has been shown to be mediated by VP1 protein via the RGD sequence. Antibodies against the RGD sequence of VP1 blocked attachment of virus to BHK cells (Fox, G., Parry, N. R., Barnett, P. V., McGinn, B., Rowland, D. J., and Brown, F. 1989. The Cell Attachment Site on Foot-and-Mouth Disease Virus Includes the Amino Acid Sequence RGD (Arginine-Glycine-Aspartic Acid) J. Gen. Virol., 70:625-637).
- 10
- 15

It has been demonstrated that bacterial adherence can be based on interaction of a bacterial adhesin RGD sequence with an integrin and that bacterial adhesins can have multiple binding site characteristic of eukaryotic extracellular matrix proteins. RGD recognition is one of the important mechanisms used by microbes to gain entry into eukaryotic cells.

20

The complete deduced protein sequence of the *Chlamydia pneumoniae* genome was searched for the presence of RGD sequence. There were a total of 54 ORFs that had one or more RGD sequences. Not all RGD containing proteins mediate cell attachment. It has been shown that RGD containing peptides that have proline immediately following the RGD sequence are inactive in cell attachment assays (Pierschbacher & Ruoslahti. 1987. Influence of stereochemistry of the sequence Arg-Gly-Asp-Xaa on binding specificity in cell adhesion. J. Biol. Chem. 262:17294-98). ORFs that had RGD, with proline as the amino acid following the RGD sequence were excluded from the list. Also, RGD sequence may not be available at the surface of the protein or may be present in a context that is not compatible with integrin binding. Since not all RGD- containing proteins are involved in cell attachment, several other criteria were used to refine the list of RGD- containing proteins. A list of ORFs in the *Chlamydia pneumoniae* genome encoding polypeptides with RGD recognition sequence(s) is in the specification.

25

30

Non-*Chlamydia trachomatis* ORFs

Chlamydia pneumoniae ORFs were compared to the ORFs in the *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value worse than e

35

¹⁰ (i.e. $>e^{-10}$) against *Chlamydia trachomatis* ORFs are included in this section. A list of ORFs in the *Chlamydia pneumoniae* genome which are not found in *Chlamydia trachomatis* is set forth above in the specification.

5 Cell Wall Anchor Surface ORFs

Many surface proteins are anchored to the cell wall of Gram-positive bacteria via the conserved LPXTG motif (Schneewind, O., Fowler, A., and Faull, K.F. 1995. Structure of the Cell Wall Anchor of Surface Proteins in *Staphylococcus aureus*. Science 268:103-106). A search of the *Chlamydia pneumoniae* ORFs was done using the motif LPXTG. A list of ORFs in the *Chlamydia*
¹⁰ *pneumoniae* genome encoding polypeptides anchored to the cell wall is in the specification.

ATCC Deposits

Samples of *Chlamydia pneumoniae* were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the accession
¹⁵ number ---. Cells can be grown, harvested and purified, and DNA can be prepared as discussed above. In order to enable recovery of specific fragments of the chromosome, one can run targeted PCR reactions, whose amplification products can then be sequenced and/or cloned into any suitable vector, according to standard procedures known to those skilled in the art.

In addition, a sample of three pools of clones covering chromosomal regions of interest
²⁰ were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the indicated accession number: —. Each pool of clones contains a series of clones. When taken together, the three pools in the sample cover a portion of the chromosome, with a redundancy of slightly more than two. The total number of clones in the sample is 196.

²⁵ The clones cover the following three regions of interest:

- (i) position 30,000 to 40,000 of SEQ ID No. 1, referred to as region A;
- (ii) position 501,500 to 557,000 of SEQ ID No. 1, referred to as region B; and
- (iii) position 815,000 to 830,000 of SEQ ID No. 1, referred to as region C.

Table 4 lists groups of oligonucleotides to be used to amplify each of ORFs 2-1291
³⁰ according to standard procedures known to those skilled in the art. Such oligonucleotides are listed as SEQ ID Nos. 1292 to 6451. For each ORF, the following is listed: one forward primer positioned 2,000 bp upstream of the beginning of the ORF; one forward primer positioned 200 bp upstream of the beginning of the ORF; one reverse primer positioned 2,000 bp downstream at the end of ORF, which is 2,000 bp upstream of the end site of the ORF on the complementary strand;
³⁵ and one reverse primer 200 bp downstream at the end of ORF, which is 200 bp upstream of the end site of the ORF on the complementary strand. The corresponding SEQ ID Nos. for the primers are listed in Table 4, where Fp is the proximal forward primer; Fd is the distal forward

primer; Bp is the proximal reverse primer; and Bd is the distal reverse primer. The positions of the 5' ends of each of these primers on the nucleotide sequence of SEQ ID No. 1 are shown in Table 5.

5 Table 6 lists oligonucleotides (SEQ ID Nos. 6452-6843) to be used to amplify the inserts of each of the 196 clones present in the pooled sample according to standard procedures well known to those of skill in the art. These primers can also be utilized to amplify the chromosomal region corresponding to the region A, B or C within which the particular insert lies. Their positions are indicated in Table 7.

10 The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

15 All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

TABLE 1							Score	I%
ORF	Begin	End	Homology	ID	Species			
ORF2	42	794	triosephosphate isomerase	L27492	<i>Thermotoga maritima</i>		567	54
ORF3	1258	1614	putative					
ORF4	1807	2418	polypeptide deformylase	D90906	<i>Synechocystis</i> sp.		316	40
ORF5	3393	2491	hypothetical protein	Z75208	<i>Bacillus subtilis</i>		338	42
ORF6	3639	4067	unknown	U87792	<i>Bacillus subtilis</i>		117	38
ORF7	5649	4270	putative					
ORF8	7463	6012	putative					
ORF9	8051	8962	putative					
ORF10	9129	9959	putative					
ORF11	10687	10361	putative					
ORF12	10927	11232	putative					
ORF13	11246	12727	amidase	U49269	<i>Moraxella catarrhalis</i>		1108	42
ORF14	12691	14190	PET112	D90913	<i>Synechocystis</i> sp.		1044	46
ORF15	14484	17249	POMP91A	U65942	<i>Chlamydia psittaci</i>		1074	43
ORF16	16039	15770	putative					
ORF17	17845	20853	putative					
ORF18	21137	22042	putative					
ORF19	22046	23476	putative					
ORF20	23681	26110	putative					
ORF21	26109	25861	putative					
ORF22	26241	26978	putative					
ORF23	26960	27754	putative					
ORF24	27747	28577	putative					
ORF25	28887	29492	POMP91A	U65942	<i>Chlamydia psittaci</i>		180	39
ORF26	29432	30028	POMP91A	U65942	<i>Chlamydia psittaci</i>		361	51
ORF27	30024	31472	POMP91A	U65942	<i>Chlamydia psittaci</i>		879	54
ORF28	31758	32288	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		144	43
ORF29	32201	33991	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		1126	48
ORF30	33852	34541	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		589	62
ORF31	34783	36063	POMP91B precursor	U65943	<i>Chlamydia psittaci</i>		469	46
ORF32	36009	37529	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		1338	51
ORF33	37881	39362	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		671	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF34	39418	39161	putative				
ORF35	39366	40715	POMP90A precursor	U65942	<i>Chlamydia psittaci</i>	904	47
ORF36	43076	41094	putative				
ORF37	43800	43066	putative				
ORF38	44828	43785	putative				
ORF39	45340	44753	homologous to unidentified E. coli protein	M96343	<i>Bacillus subtilis</i>	136	44
ORF40	45752	45372	o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES HAEIN SW: P44808	AE000184	<i>Escherichia coli</i>	269	43
ORF41	46996	45701	ABC transporter, ATP-binding protein (yheS)	AE000596	<i>Helicobacter pylori</i>	878	39
ORF42	47961	47569	putative				
ORF43	48960	48040	hypothetical protein	D64001	<i>Synechocystis sp.</i>	404	37
ORF44	51452	50133	Lon protease-like protein	X74215	<i>Homo sapiens</i>	1232	54
ORF45	52606	51335	unknown	Z54285	<i>Schizosaccharomyces pombe</i>	781	47
ORF46	53684	53319	putative				
ORF47	54195	53746	putative				
ORF48	55278	56453	heat-shock protein	U15010	<i>Legionella pneumophila</i>	975	45
ORF49	56493	57266	branched chain alpha-keto acid dehydrogenase E1-alpha	M97391	<i>Bacillus subtilis</i>	329	36
ORF50	57297	58526	branched chain alpha-keto acid dehydrogenase E1-beta	M97391	<i>Bacillus subtilis</i>	707	50
ORF51	59851	58565	putative				
ORF52	61495	59924	ComE	D90903	<i>Synechocystis sp.</i>	134	55
ORF53	61324	62151	putative				
ORF54	62132	62470	Hpr protein	X12832	<i>Bacillus subtilis</i>	136	36
ORF55	62474	63733	enzyme I (ptsI)	U32844	<i>Haemophilus influenzae</i>	381	35
ORF56	63881	64186	f831; This 831 aa orf is 46 pct identical (11 gaps) to 709 residues of an approx. 712 aa protein PT1A ECOLI SW: P32670	AE000326	<i>Escherichia coli</i>	123	34
ORF57	64611	64318	ORF107	X17014	<i>Bacillus subtilis</i>	128	33
ORF58	65485	64673	putative				
ORF59	65999	65301	dnaZX-like ORF put. DNA polymerase III	X06803	<i>Bacillus subtilis</i>	596	52

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF60	66244	67281	putative				
ORF61	67265	67699	putative				
ORF62	67703	68539	putative				
ORF63	68805	70736	putative				
ORF64	69172	68831	putative				
ORF65	70642	71142	putative				
ORF66	71325	72029	putative				
ORF67	72060	73637	putative				
ORF68	74061	76175	YqfF	D84432	<i>Bacillus subtilis</i>	542	44
ORF69	78351	77680	porphobilinogen deaminase	D28503	<i>Clostridium josui</i>	262	42
ORF70	79356	78355	sms protein	D90914	<i>Synechocystis</i> sp.	736	52
ORF71	79983	79693	ribonuclease III (mc)	AE000579	<i>Helicobacter pylori</i>	98	33
ORF72	80441	79938	ORF3	D64116	<i>Bacillus subtilis</i>	268	44
ORF73	80475	80969	putative				
ORF74	81296	83080	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	893	38
ORF75	83291	83932	manganese superoxide dismutase	X77021	<i>Caenorhabditis elegans</i>	622	58
ORF76	84005	84769	acetyl-CoA carboxylase beta subunit (accD)	AE000604	<i>Helicobacter pylori</i>	602	50
ORF77	84975	85244	deoxyuridinetriphosphatase (dut)	U32776	<i>Haemophilus influenzae</i>	110	41
ORF78	85123	85425	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	AE000596	<i>Helicobacter pylori</i>	265	68
ORF79	85397	85903	ORF2	L26916	<i>Pseudomonas aeruginosa</i>	173	34
ORF80	85909	86583	enzyme IIANtr	U18997	<i>Escherichia coli</i>	170	42
ORF81	86626	88065	putative				
ORF82	89257	91026	putative				
ORF83	91291	93030	putative				
ORF84	93295	94086	putative				
ORF85	95285	94707	putative				
ORF86	95667	96557	putative				
ORF87	96317	97456	putative				
ORF88	98435	97968	putative				
ORF89	99460	98426	putative				
ORF90	100144	101325	elongation factor Tu	L22216	<i>Chlamydia trachomatis</i>	1917	95

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF91	101457	101720	putative				
ORF92	101704	102273	transcription factor	L10348	<i>Thermus aquaticus thermophilus</i>	376	49
ORF93	102356	102805	ribosomal protein L11	D13303	<i>Bacillus subtilis</i>	458	63
ORF94	102835	103530	ribosomal protein L1	Z11839	<i>Thermotoga maritima</i>	642	51
ORF95	103549	104058	ribosomal protein L10	M89911	<i>Streptomyces antibioticus</i>	82	31
ORF96	104096	104491	rp112 (AA 1-128)	X53178	<i>Synechocystis PCC6803</i>	325	47
ORF97	104601	108386	DNA-directed RNA polymerase beta chain	X64172	<i>Staphylococcus aureus</i>	2740	52
ORF98	108401	112054	rpoC	V00339	<i>Escherichia coli</i>	2947	54
ORF99	112033	112590	acetylornithine deacetylase (EC 5.1.1.16)	M22622	<i>Leptospira biflexa</i>	514	62
ORF100	112672	113682	transaldolase	L19437	<i>Homo sapiens</i>	755	49
ORF101	113726	114121	putative				
ORF102	114711	114136	putative				
ORF103	115267	115755	putative				
ORF104	115911	116543	putative				
ORF105	116736	118055	ATPase alpha-subunit	X63855	<i>Thermus aquaticus thermophilus</i>	934	50
ORF106	117968	118522	adenosine triphosphatase A subunit	D50528	<i>Acetabularia acetabulum</i>	147	32
ORF107	118530	119843	V-ATPase B subunit	U96487	<i>Desulfurococcus sp. SY</i>	751	48
ORF108	119816	120457	putative				
ORF109	120451	122430	v-type Na-ATPase	X76913	<i>Enterococcus hirae</i>	264	35
ORF110	122504	122950	ATP synthase, subunit K	U67478	<i>Melhanococcus jannaschii</i>	184	31
ORF111	123528	126347	valyl-tRNA synthetase	X05891	<i>Escherichia coli</i>	1679	49
ORF112	126332	129166	protein kinase-like protein	U19250	<i>Streptomyces coelicolor</i>	427	37
ORF113	134690	129213	UvrA	D49911	<i>Thermus thermophilus</i>	3107	41
ORF114	134925	136382	pyruvate kinase	U83196	<i>Chlamydia trachomatis</i>	1748	71
ORF115	137870	136482	HtrB protein	X61000	<i>Escherichia coli</i>	147	38
ORF116	137899	138240	putative				
ORF117	138239	137928	putative				
ORF118	139558	138257	putative				
ORF119	140352	139516	YbbP	AB002150	<i>Bacillus subtilis</i>	231	46
ORF120	140498	141841	cyanide insensitive terminal oxidase	Y10528	<i>Pseudomonas aeruginosa</i>	538	50
ORF121	141855	142658	cyanide insensitive terminal oxidase	Y10528	<i>Pseudomonas aeruginosa</i>	310	40
ORF122	144258	143050	putative				
ORF123	145258	144494	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF124	14544	146749	product similar to E. coli PhoH protein	Z97025	<i>Bacillus subtilis</i>	836	47
ORF125	147318	146767	putative				
ORF126	148261	147677	putative				
ORF127	149029	152157	isoleucyl-tRNA synthetase	U04953	<i>Homo sapiens</i>	2361	52
ORF128	154108	152201	leader peptidase I	D90904	<i>Synechocystis sp.</i>	225	47
ORF129	155135	154308	putative				
ORF130	155141	155467	YtiA	AF008220	<i>Bacillus subtilis</i>	201	43
ORF131	155703	156779	orf 361; ranslated orf similarity to SW: RF1 SALT peptide chain release factor 1 of <i>Salmonella typhimurium</i>	X78969	<i>Coxiella burnetii</i>	863	59
ORF132	156748	157635	product similar to E.coli PRFA2 protein	Z49782	<i>Bacillus subtilis</i>	144	37
ORF133	157653	158996	Ffh	U82109	<i>Thermus aquaticus</i>	797	45
ORF134	159363	159986	tRNA (guanine-N1)-methyltransferase (trmD)	U32705	<i>Haemophilus influenzae</i>	545	49
ORF135	159880	160446	putative				
ORF136	160477	160839	ribosomal protein L19	X72627	<i>Synechocystis sp.</i>	319	50
ORF137	160898	161539	putative protein highly homologous to E. coli RNase HII	D32253	<i>Magnetospirillum sp.</i>	427	49
ORF138	161527	162153	5'guanylate kinase (gmk)	U32848	<i>Haemophilus influenzae</i>	385	43
ORF139	162144	162443	putative				
ORF140	162437	164098	methionyl-tRNA synthetase	AB004537	<i>Schizosaccharomyces pombe</i>	861	54
ORF141	165451	164228	exodeoxyribonuclease V (recD)	U32811	<i>Haemophilus influenzae</i>	432	32
ORF142	166349	165411	putative				
ORF143	166949	168442	putative				
ORF144	169416	171029	putative				
ORF145	170857	171459	putative				
ORF146	172652	173428	putative biotin-protein ligase	Z97992	<i>Schizosaccharomyces pombe</i>	292	44
ORF147	174626	173439	putative				
ORF148	174816	175613	putative				
ORF149	175598	175954	putative				
ORF150	175958	176935	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF151	177708	176938	orf 3' of chaperonin homolog hypB [Chlamydia psittaci, pigeon strain P-1041, Peptide Partial, 98 aa]	S40172	<i>Chlamydia psittaci</i>	376	74
ORF152	177128	177376	putative				
ORF153	179472	177841	putative	M69217	<i>Chlamydia pneumoniae</i>	2678	100
ORF154	179822	179517	putative	M69217	<i>Chlamydia pneumoniae</i>	498	99
ORF155	181793	179943	Pz-peptidase	D88209	<i>Bacillus licheniformis</i>	1088	38
ORF156	182628	181876	o247; This 247 aa orf is 51 pct identical (0 gaps) to 117 residues of an approx. 160 aa protein YPH7 CHRVI SW: P45371	AE000174	<i>Escherichia coli</i>	401	42
ORF157	184420	183074	glutamate-1-semialdehyde 2,1- aminomutase	X53696	<i>Escherichia coli</i>	823	41
ORF158	184988	184467	ORF o211	U28377	<i>Escherichia coli</i>	87	54
ORF159	185483	185112	hypothetical protein	D90906	<i>Synechocystis sp.</i>	91	33
ORF160	185902	185483	ribose 5-phosphate isomerase	U28377	<i>Escherichia coli</i>	111	41
ORF161	186174	185839	ribose 5-phosphate isomerase A (SP:P27252)	U32729	<i>Haemophilus influenzae</i>	190	46
ORF162	187720	186587	hypothetical	D83026	<i>Bacillus subtilis</i>	536	42
ORF163	188318	190933	ATP-dependent protease binding subunit	M29364	<i>Escherichia coli</i>	2010	53
ORF164	191090	191635	putative				
ORF165	191547	192743	putative				
ORF166	192969	193469	putative				
ORF167	194044	193610	putative				
ORF168	194196	195809	unknown				
ORF169	196088	198073	DNA ligase (EC 6.5.1.2)	Z84395	<i>Mycobacterium tuberculosis</i>	242	52
ORF170	198132	199454	putative	M24278	<i>Escherichia coli</i>	1317	46
ORF171	199351	202818	putative				
ORF172	204552	202999	PcpB	U60175	<i>Sphingomonas chlorophenolica</i>	80	41
ORF173	205648	204692	putative				
ORF174	205807	207327	leucine tRNA synthetase	AF008220	<i>Bacillus subtilis</i>	1595	57
ORF175	207182	207775	leucyl-tRNA synthetase	X06331	<i>Escherichia coli</i>	363	51
ORF176	207779	208267	transfer RNA-Leu synthetase	M88581	<i>Bacillus subtilis</i>	285	43
ORF177	208267	209577	KDO transferase	Z31593	<i>Chlamydia pneumoniae</i>	2262	100

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF178	211807	211271	KDO-transferase	X80061	<i>Chlamydia psittaci</i>	105	38
ORF179	212188	211844	putative				
ORF180	214079	212448	pyrophosphate-dependent phosphofructokinase beta subunit	Z32850	<i>Ricinus communis</i>	1003	45
ORF181	214907	214083	CinI	U44893	<i>Butyrivibrio fibrisolvens</i>	111	41
ORF182	216154	215429	putative				
ORF183	216115	216678	putative				
ORF184	216728	217282	putative				
ORF185	217267	217866	putative				
ORF186	218593	218261	putative				
ORF187	219821	218994	putative				
ORF188	221382	220309	putative				
ORF189	222719	221433	GMP synthetase	M10101	<i>Escherichia coli</i>	1151	48
ORF190	223521	222724	IMP dehydrogenase	X66859	<i>Acinetobacter calcoaceticus</i>	778	58
ORF191	224499	225008	putative				
ORF192	225140	225559	putative				
ORF193	225555	226802	putative				
ORF194	227800	226892	putative				
ORF195	228335	228072	putative				
ORF196	229251	228643	putative				
ORF197	230983	229622	YqhX	D84432	<i>Bacillus subtilis</i>	1386	56
ORF198	231483	230983	acetyl-CoA carboxylase biotin carboxyl carrier protein	U38804	<i>Porphyra purpurea</i>	199	52
ORF199	232063	231509	elongation factor P	D64001	<i>Synechocystis sp.</i>	282	32
ORF200	232739	232053	pentose-5-phosphate-3-epimerase	D90911	<i>Synechocystis sp.</i>	463	43
ORF201	233166	234356	putative				
ORF202	233518	233165	putative				
ORF203	234536	235186	ORF2	L35036	<i>Chlamydia psittaci</i>	570	60
ORF204	235379	236689	putative				
ORF205	236680	237618	putative				
ORF206	237521	238345	putative				
ORF207	238281	238973	putative				
ORF208	238871	240115	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF209	240191	241564	putative				
ORF210	242281	241604	YqiZ	D84432	<i>Bacillus subtilis</i>	379	39
ORF211	242933	242274	f222; This 222 aa orf is 48 pct identical (0 gaps) to 208 residues of an approx. 232 aa protein YCKA_BACSU.SW.P42399	AE000284	<i>Escherichia coli</i>	382	45
ORF212	243416	242976	arginine repressor protein (argR)	U32800	<i>Haemophilus influenzae</i>	229	46
ORF213	243500	244531	sialoglycoprotease	U15958	<i>Pasteurella haemolytica</i>	565	53
ORF214	244480	246021	oligopeptide permease homolog AII	AF000366	<i>Borrelia burgdorferi</i>	457	34
ORF215	246330	247811	OppAIV	AF000948	<i>Borrelia burgdorferi</i>	453	35
ORF216	247831	249174	OppA gene product	X56347	<i>Bacillus subtilis</i>	255	37
ORF217	249437	251038	dcIAE	X56678	<i>Bacillus subtilis</i>	469	37
ORF218	251325	252212	OppB gene product	X56347	<i>Bacillus subtilis</i>	652	42
ORF219	253156	254007	oligopeptidepermease	X89237	<i>Streptococcus pyogenes</i>	574	48
ORF220	253974	254852	ATP binding protein	L18760	<i>Lactococcus lactis</i>	433	40
ORF221	255258	256094	KDO-transferase	X80061	<i>Chlamydia psittaci</i>	106	46
ORF222	256640	257455	putative				
ORF223	257502	258239	2-OXOGLUTARAT	A47930	<i>Spinacia oleracea</i>	636	52
ORF224	257869	257501	putative				
ORF225	259248	260897	pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit	M55191	<i>Solanum tuberosum</i>	1055	44
ORF226	262753	261788	putative				
ORF227	263059	262757	putative				
ORF228	264375	263182	putative				
ORF229	265985	264747	putative				
ORF230	266637	266059	putative				
ORF231	267338	266538	putative				
ORF232	267922	267473	putative				
ORF233	269647	270771	tRNA guanine transglycosylase	L33777	<i>Zymomonas mobilis</i>	628	44
ORF234	272777	273145	ORF 4	D00624	<i>Bacteriophage chp1</i>	100	41
ORF235	273253	273636	putative				
ORF236	273705	273977	putative				
ORF237	276016	275717	putative				
ORF238	276439	276020	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF239	276792	277253	putative				
ORF240	277318	277599	putative				
ORF241	278578	277877	putative				
ORF242	279258	278554	FbpC	U33937	<i>Neisseria gonorrhoeae</i>	312	39
ORF243	280435	279533	putative				
ORF244	281547	280849	putative				
ORF245	281696	282325	CMP-2-keto-3-deoxyoctulosonic acid synthetase	U15192	<i>Chlamydia trachomatis</i>	637	63
ORF246	282459	284069	CTP synthetase	U15192	<i>Chlamydia trachomatis</i>	2000	68
ORF247	284056	284517	ORF3	U15192	<i>Chlamydia trachomatis</i>	453	65
ORF248	284606	285775	glucose 6-phosphate dehydrogenase	U83195	<i>Chlamydia trachomatis</i>	1263	77
ORF249	285592	285987	glucose 6-phosphate dehydrogenase	U83195	<i>Chlamydia trachomatis</i>	519	79
ORF250	286179	286976	glucose-6-phosphate dehydrogenase isozyme	D88189	<i>Acinobacillus actinomycetemcomitans</i>	216	40
ORF251	287583	287002	putative				
ORF252	287951	287451	putative				
ORF253	288499	288816	putative				
ORF254	289674	288505	putative				
ORF255	288839	289213	putative				
ORF256	289970	290254	putative				
ORF257	291931	292803	gamma-D-glutamyl-L-diamino acid endopeptidase II	XG4809	<i>Bacillus sphaericus</i>	95	39
ORF258	293258	292755	ScoS9	U43429	<i>Streptomyces coelicolor</i>	233	45
ORF259	293718	293272	ribosomal protein L13 (rpL13)	U32823	<i>Haemophilus influenzae</i>	364	47
ORF260	294630	293953	glutamine transport ATP-binding protein Q	U67524	<i>Melhanococcus jannaschii</i>	387	46
ORF261	296153	294636	putative				
ORF262	294817	295068	putative				
ORF263	296354	297862	conserved hypothetical protein	AE000586	<i>Helicobacter pylori</i>	641	46
ORF264	298415	297879	putative				
ORF265	298777	298253	putative				
ORF266	299572	298781	putative				
ORF267	300487	299633	putative				
ORF268	301586	300702	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF269	302440	301571	putative				
ORF270	302838	302437	putative				
ORF271	303335	302745	putative				
ORF272	304394	303852	putative				
ORF273	304606	305223	f311; This 311 aa orf is 22 pct identical (13 gaps) to 186 residues of an approx. 488 aa protein YACA_BACSU SW: P37563; pyu1 of D21139	AE000232	<i>Escherichia coli</i>	250	38
ORF274	305394	306236	survival protein surE	U81296	<i>Sinorhizobium meliloti</i>	156	42
ORF275	306501	307439	YqfU	D84432	<i>Bacillus subtilis</i>	547	42
ORF276	308033	307458	3-octaprenyl-4-hydroxybenzoate carboxylase	U61168	<i>Bacillus firmus</i>	403	42
ORF277	308924	308037	4-hydroxybenzoate octaprenyltransferase	U61168	<i>Bacillus firmus</i>	152	40
ORF278	309485	310180	putative				
ORF279	310426	311214	putative				
ORF280	311597	311253	putative				
ORF281	312772	311780	putative				
ORF282	313425	312772	putative				
ORF283	313646	313377	putative				
ORF284	313937	314665	lysophospholipase homolog	AF006678	<i>Schistosoma mansoni</i>	141	44
ORF285	315576	314755	dnaZX	X17014	<i>Bacillus subtilis</i>	154	39
ORF286	316157	315531	unknown	D26185	<i>Bacillus subtilis</i>	284	31
ORF287	318657	316156	DNA gyrase	L47978	<i>Aeromonas salmonicida</i>	1785	48
ORF288	321042	318676	DNA gyrase subunit B	U35453	<i>Clostridium acetobutylicum</i>	1838	59
ORF289	321445	321098	putative				
ORF290	322309	321710	putative				
ORF291	323190	322366	outer membrane protein	AE000654	<i>Helicobacter pylori</i>	376	43
ORF292	323843	323181	hypothetical	U70214	<i>Escherichia coli</i>	356	37
ORF293	324878	323856	ATP-binding protein (abc)	U32744	<i>Haemophilus influenzae</i>	545	44
ORF294	325340	326410	f374; This 374 aa orf is 30 pct identical (9 gaps) to 102 residues of an approx. 512 aa protein FLIC SALMU SW: P06177	AE000299	<i>Escherichia coli</i>	1194	62
ORF295	326433	327836	Xas A	AE000246	<i>Escherichia coli</i>	479	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF296	328465	327839	putative				
ORF297	329360	328857	putative				
ORF298	330907	329357	putative				
ORF299	332455	330956	MgtE	U18744	<i>Bacillus firmus</i>	203	36
ORF300	334536	332395	putative				
ORF301	336091	334877	putative				
ORF302	336103	337302	putative				
ORF303	338129	338830	putative				
ORF304	338965	339501	putative				
ORF305	339508	340143	putative				
ORF306	340247	342967	putative				
ORF307	343385	343810	cAMP-dependent protein kinase type I regulatory subunit	U75932	<i>Rattus norvegicus</i>	102	37
ORF308	344171	343935	acyl carrier protein (acpP)	AE000570	<i>Helicobacter pylori</i>	198	55
ORF309	345082	344330	3-ketoacyl-ACP reductase	U39441	<i>Vibrio harveyi</i>	598	48
ORF310	346005	345082	malonyl-CoA:Acyl carrier protein transacylase	U59433	<i>Bacillus subtilis</i>	538	45
ORF311	346784	346437	beta-ketoacyl-acyl carrier protein synthase III (fabH)	AE000540	<i>Helicobacter pylori</i>	273	50
ORF312	347029	346715	beta-ketoacyl-acyl carrier protein synthase III	M77744	<i>Escherichia coli</i>	265	63
ORF313	347034	347723	recombination protein	D90916	<i>Synechocystis sp.</i>	363	42
ORF314	348075	350459	putative				
ORF315	350598	351071	putative				
ORF316	351075	352175	rifampicin resistance protein	L22690	<i>Rickettsia rickettsii</i>	495	46
ORF317	353291	352230	putative				
ORF318	353442	354467	pyruvate dehydrogenase E1 component, alpha subunit	D90915	<i>Synechocystis sp.</i>	571	44
ORF319	354451	354933	pyruvate dehydrogenase E1 beta subunit	U09137	<i>Arabidopsis thaliana</i>	495	59
ORF320	355000	355449	pyruvate dehydrogenase E1 component, beta subunit	U38804	<i>Porphyras purpurea</i>	336	47
ORF321	355448	356743	F23B12.5	Z77659	<i>Caenorhabditis elegans</i>	759	46
ORF322	355953	355642	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF323	359310	356827	glycogen phosphorylase B	U47025	<i>Homo sapiens</i>	2193	57
ORF324	359120	359377	putative				
ORF325	359525	359908	putative				
ORF326	361290	359947	DnaA	D89066	<i>Staphylococcus aureus</i>	375	46
ORF327	363785	361362	hypothetical	U32781	<i>Haemophilus influenzae</i>	394	44
ORF328	364496	363888	putative				
ORF329	364832	365290	putative				
ORF330	365304	365669	dpi	M76470	<i>Escherichia coli</i>	160	45
ORF331	366599	365667	NADPH thioredoxin reductase	AC002329	<i>Arabidopsis thaliana</i>	975	60
ORF332	367291	369030	ribosomal protein S1 (rpS1)	U32801	<i>Haemophilus influenzae</i>	1209	41
ORF333	369134	369808	NusA	U74759	<i>Chlamydia trachomatis</i>	995	87
ORF334	369917	370438	NusA	U74759	<i>Chlamydia trachomatis</i>	760	87
ORF335	370365	372647		U74759	<i>Chlamydia trachomatis</i>	2173	61
ORF336	372557	373066	initiation factor IF2-beta (infB; gbg start codon)	X00513	<i>Escherichia coli</i>	333	39
ORF337	373020	373442	ORF6 gene product	Z18631	<i>Bacillus subtilis</i>	192	34
ORF338	373467	374195	tRNA pseudouridine 55 synthase	D90917	<i>Synechocystis sp.</i>	358	47
ORF339	374176	375099	hypothetical 34.6 kD protein in rpsT-ileS intergenic region	AE000113	<i>Escherichia coli</i>	395	39
ORF340	375676	375083	hypothetical GTP-binding protein in pth 3' region	AE000219	<i>Escherichia coli</i>	507	53
ORF341	376173	375634	hypothetical	U32723	<i>Haemophilus influenzae</i>	480	59
ORF342	376564	377643	YscU	U08019	<i>Yersinia enterocolitica</i>	538	37
ORF343	377956	379773	lcrD gene product	X67771	<i>Yersinia enterocolitica</i>	1302	47
ORF344	379781	380425	putative				
ORF345	380281	381000	putative				
ORF346	381008	381460	putative				
ORF347	381460	383037	4-alpha-glucanotransferase	L37874	<i>Clostridium butyricum</i>	302	38
ORF348	383257	383523	ribosomal protein L28 (rpL28)	U32776	<i>Haemophilus influenzae</i>	175	55
ORF349	383553	385304	hypothetical protein	D90901	<i>Synechocystis sp.</i>	565	38
ORF350	385397	386458	comE ORF-I	D64002	<i>Synechocystis sp.</i>	187	10
ORF351	387242	386514	putative				
ORF352	388764	387013	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF353	390120	390932	methylentetrahydrofolate dehydrogenase	D64000	<i>Synechocystis sp.</i>	588	53
ORF354	390919	391818	f351; Residues 1-121 are 100 pct identical to YOJL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOJK_ECOLI SW: P33943	AE000310	<i>Escherichia coli</i>	186	39
ORF355	392379	391885	small protein	D90914	<i>Synechocystis sp.</i>	387	46
ORF356	392582	392986	putative				
ORF357	392776	393684	putative				
ORF358	394151	394804	RecF protein	D90907	<i>Synechocystis sp.</i>	232	34
ORF359	394928	395308	putative				
ORF360	395259	395990	putative				
ORF361	397815	395953	hypothetical	U32773	<i>Haemophilus influenzae</i>	391	36
ORF362	398850	397831	H. influenzae predicted coding region HI0807	U32763	<i>Haemophilus influenzae</i>	580	39
ORF363	400085	399099	putative				
ORF364	401245	400073	YtgC	AF008220	<i>Bacillus subtilis</i>	244	30
ORF365	401474	401136	putative				
ORF366	402199	401423	unknown	U52850	<i>Erysipelothrix rhusiopathiae</i>	534	46
ORF367	403193	402186	putative				
ORF368	403650	404165	putative				
ORF369	404343	405914	adenine nucleotide translocase	Z49227	<i>Arabidopsis thaliana</i>	1280	55
ORF370	405984	407327	putative				
ORF371	407712	408806	putative				
ORF372	410439	409075	putative				
ORF373	411826	410954	putative				
ORF374	412482	414302	lepA gene product	X91655	<i>Bacillus subtilis</i>	1827	59
ORF375	415402	414407	6-phosphogluconate dehydrogenase, decarboxylating (gmd)	U32737	<i>Haemophilus influenzae</i>	687	51
ORF376	415848	415237	6-phosphogluconate dehydrogenase, 6PGD [Ceratitis capitata=medflies, Peptide, 481 aa]	S67873	<i>Ceratitis capitata</i>	695	64
ORF377	417131	415866	tyrosyl-tRNA synthetase (tyrS)	J01719	<i>Escherichia coli</i>	821	45
ORF378	417258	417566	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF379	418326	417454	whiG-Stv gene product	X68709	<i>Sireptovorticillium griseocarneum</i>	464	41
ORF380	420057	418426	FLHA gene product	X63698	<i>Bacillus subtilis</i>	455	49
ORF381	420448	420720	ferredoxin IV	M59855	<i>Rhodobacter capsulatus</i>	174	63
ORF382	420980	421552	putative				
ORF383	421556	422029	putative				
ORF384	422461	422925	putative				
ORF385	423562	424320	putative				
ORF386	424250	424591	putative				
ORF387	424830	426047	putative				
ORF388	426240	427397	putative				
ORF389	428841	430703	GopE	D90908	<i>Synechocystis sp.</i>	877	47
ORF390	430694	431446	YfiH	U50134	<i>Escherichia coli</i>	136	35
ORF391	431597	432100	putative				
ORF392	432165	432779	putative				
ORF393	433272	432832	dihydrolipoamide succinyltransferase (sucB)	U32839	<i>Haemophilus influenzae</i>	475	64
ORF394	433925	433227	dihydrolipoamide succinyltransferase (sucB)	U32839	<i>Haemophilus influenzae</i>	332	45
ORF395	436678	433934	alpha-ketoglutarate dehydrogenase	U41762	<i>Rhodobacter capsulatus</i>	1530	44
ORF396	437176	438357	oxygen-independent coproporphyrinogen III oxidase (hemN)	AE000628	<i>Helicobacter pylori</i>	442	42
ORF397	440317	438518	putative				
ORF398	440001	440345	putative				
ORF399	441233	440517	ORF f286	U18997	<i>Escherichia coli</i>	168	45
ORF400	440719	441012	putative				
ORF401	442192	441230	putative				
ORF402	442888	442343	putative				
ORF403	442371	442961	putative				
ORF404	443578	443003	[karp] gene products	M86605	<i>Chlamydia trachomatis</i>	505	78
ORF405	444500	443526	aminopeptidase	D17450	<i>Mycoplasma salivarium</i>	273	39
ORF406	444842	444528	putative				
ORF407	445009	444743	putative	L39923	<i>Mycobacterium leprae</i>	133	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF408	445718	445182	putative				
ORF409	445807	447804	Sulp	U18908	<i>Zea mays</i>	1307	52
ORF410	448738	447803	putative				
ORF411	449628	448618	RuvB protein	U38840	<i>Thermotoga maritima</i>	845	53
ORF412	450298	450867	deoxycytidine triphosphate deaminase (dcd)	AE000554	<i>Helicobacter pylori</i>	573	58
ORF413	450713	451207	putative				
ORF414	451211	452452	hemolysin	D90914	<i>Synechocystis sp.</i>	227	39
ORF415	452448	453659	similar to [SwissProt Accession Number P37908]	D90888	<i>Escherichia coli</i>	96	33
ORF416	454843	453725	NifS gene product	L34879	<i>Anabaena azollae</i>	533	38
ORF417	455608	454865	hypothetical protein	D90908	<i>Synechocystis sp.</i>	371	36
ORF418	456243	457007	putative				
ORF419	457016	457708	putative				
ORF420	458368	457979	unknown	D26185	<i>Bacillus subtilis</i>	152	36
ORF421	459496	458372	mutY homolog	U63329	<i>Homo sapiens</i>	466	46
ORF422	459493	460194	hypothetical protein	D90914	<i>Synechocystis sp.</i>	98	38
ORF423	461446	460355	putative				
ORF424	462298	461450	putative				
ORF425	462444	463349	enoyl-ACP reductase	Y13861	<i>Nicotiana tabacum</i>	1008	69
ORF426	464241	463342	putative				
ORF427	464574	465065	putative				
ORF428	465129	465611	putative				
ORF429	465571	466317	putative				
ORF430	466317	467093	H. pylori predicted coding region HP0152	AE000536	<i>Helicobacter pylori</i>	246	36
ORF431	466999	467502	putative				
ORF432	469691	467715	unidentified transporter-ATP binding	Z82044	<i>Bacillus subtilis</i>	496	45
ORF433	470691	469660	acetyl-CoA carboxylase subunit	AF008220	<i>Bacillus subtilis</i>	781	52
ORF434	472010	470709	putative				
ORF435	471545	471799	putative				
ORF436	472359	472045	putative				
ORF437	473523	472732	orf1	X75413	<i>Escherichia coli</i>	313	42
ORF438	474889	473441	murE gene product	Z15056	<i>Bacillus subtilis</i>	679	37
ORF439	477323	475365	penicillin-binding protein 2	X59630	<i>Neisseria meningitidis</i>	451	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF440	478496	477597	hypothetical protein	D90906	<i>Synechocystis sp.</i>	534	52
ORF441	478722	479273	putative				
ORF442	479277	479705	putative				
ORF443	480050	481450	chromosomal replication initiator protein	D90909	<i>Synechocystis sp.</i>	793	40
ORF444	481469	482053	DnaA	U35673	<i>Borrelia burgdorferi</i>	157	37
ORF445	482600	482025	OrfH				
ORF446	482654	484204	putative				
			NADH:ubiquinone oxidoreductase subunit	Z37111	<i>Vibrio alginolyticus</i>	801	49
			B				
ORF447	484211	485170	NADH:ubiquinone oxidoreductase (GP:Z37111 4)	U32702	<i>Haemophilus influenzae</i>	258	48
ORF448	485170	485838	NADH:ubiquinone oxidoreductase	Z37111	<i>Vibrio alginolyticus</i>	543	55
ORF449	485813	486580	unidentified protein of Na ⁺ -translocating	D49364	<i>Vibrio alginolyticus</i>	488	48
			NADH-quinone reductase				
ORF450	486976	486638	putative				
ORF451	489071	487764	putative				
ORF452	489341	489090	putative				
ORF453	489958	489152	putative				
ORF454	490549	489962	putative				
ORF455	491163	490522	putative				
ORF456	491396	491112	putative				
ORF457	492121	491390	putative				
ORF458	492304	494838	ClpC adenosine triphosphatase	U02604	<i>Bacillus subtilis</i>	2370	46
ORF459	495943	494822	hypothetical protein in purB 5' region	AE000213	<i>Escherichia coli</i>	927	53
ORF460	496011	496565	putative				
ORF461	496569	497228	putative				
ORF462	497358	497834	putative				
ORF463	497770	498327	putative				
ORF464	499209	499589	putative				
ORF465	499520	499792	putative				
ORF466	500774	504169	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1215	45
ORF467	504139	504600	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	319	47
ORF468	504865	506877	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	992	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF469	506790	507671	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	739	46
ORF470	507718	510507	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1813	42
ORF471	508325	507912	putative				
ORF472	510660	513440	POMP90A precursor	U65942	<i>Chlamydia psittaci</i>	1830	46
ORF473	514965	513787	hypothetical	D83026	<i>Bacillus subtilis</i>	482	48
ORF474	517347	515419	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1554	51
ORF475	517058	517363	putative				
ORF476	517798	517277	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	222	41
ORF477	518200	517847	POMP91B precursor	U65943	<i>Chlamydia psittaci</i>	162	42
ORF478	518300	521146	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1900	45
ORF479	521392	522948	POMP91A	U65942	<i>Chlamydia psittaci</i>	490	39
ORF480	523244	524809	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	507	35
ORF481	524379	524125	putative				
ORF482	524649	526238	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	969	41
ORF483	526265	527104	putative				
ORF484	526947	526702	putative				
ORF485	526975	528450	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	197	48
ORF486	528408	529199	putative outer membrane protein	U72499	<i>Chlamydia psittaci</i>	154	37
ORF487	530612	529542	putative				
ORF488	531656	530616	putative				
ORF489	533974	532067	putative				
ORF490	536432	534324	putative				
ORF491	537150	536707	putative				
ORF492	537928	537080	putative				
ORF493	538438	537932	putative				
ORF494	538737	538333	putative				
ORF495	539594	539127	putative				
ORF496	541215	539590	putative				
ORF497	542571	541282	putative				
ORF498	543014	542457	putative				
ORF499	543369	542962	putative				
ORF500	543809	546628	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	506	89
ORF501	546619	549525	POMP91A	U65942	<i>Chlamydia psittaci</i>	128	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF502	547293	546994	putative				
ORF503	549699	550523	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	96	32
ORF504	550490	551551	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	223	33
ORF505	551448	552623	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	139	46
ORF506	552652	555117	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	487	48
ORF507	555029	555493	putative				
ORF508	558006	555673	putative				
ORF509	559694	558162	putative				
ORF510	558208	558573	putative				
ORF511	561692	559899	putative				
ORF512	561412	561708	putative				
ORF513	563942	561777	1,4-alpha-glucan branching enzyme	X73903	<i>Streptomyces coelicolor</i>	1743	45
ORF514	564969	563950	putative				
ORF515	566204	564936	YqeV	D84432	<i>Bacillus subtilis</i>	639	38
ORF516	567717	566302	putative GTPase required for high frequency lysogenization by bacteriophage lambda	U00005	<i>Escherichia coli</i>	686	41
ORF517	568526	567708	putative				
ORF518	569467	568742	putative				
ORF519	571065	569431	putative				
ORF520	571828	571118	arginine-binding periplasmic protein 1 precursor	AE000188	<i>Escherichia coli</i>	197	45
ORF521	572202	573308	putative				
ORF522	573146	575056	putative				
ORF523	575023	575916	carboxysome formation protein	D90901	<i>Synechocystis sp.</i>	557	59
ORF524	577891	576497	putative				
ORF525	578914	578204	putative				
ORF526	579924	578857	putative				
ORF527	580187	579858	protein kinase C inhibitor	D90906	<i>Synechocystis sp.</i>	260	49
ORF528	580017	580406	putative				
ORF529	581086	580187	Yer156cp	U18917	<i>Saccharomyces cerevisiae</i>	176	34
ORF530	581367	581828	putative				
ORF531	581678	582367	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF532	582361	583428	putative				
ORF533	584690	583431	putative				
ORF534	585237	584950	putative				
ORF535	585626	586888	hypothetical protein	D64004	<i>Synechocystis sp.</i>	805	45
ORF536	586846	587907	putative				
ORF537	589049	588180	putative				
ORF538	590500	589301	putative				
ORF539	590755	592458	aminoacyl-tRNA synthetase	L25105	<i>Chlamydia trachomatis</i>	2125	71
ORF540	592526	592903	has homology to putative heat shock proteins of <i>Bacillus subtilis</i> and <i>Clostridium acetobutylicum</i> ; ORF A; putative	L25105	<i>Chlamydia trachomatis</i>	324	59
ORF541	592836	593747	Possible negative regulator of CIRCE element; Homologs in <i>B. subtilis</i> and <i>Clostridia</i> spp. referred to as hrcA or orfA	U52216	<i>Chlamydia trachomatis</i>	960	65
ORF542	593747	594298	grpE	M62819	<i>Chlamydia trachomatis</i>	661	71
ORF543	594331	595947	DnaK protein homolog; 71,550 Da; putative	M69227	<i>Chlamydia pneumoniae</i>	2619	100
ORF544	595905	596309	DnaK protein homolog; 71,550 Da; putative	M69227	<i>Chlamydia pneumoniae</i>	674	100
ORF545	596514	597215	putative				
ORF546	597184	597957	vacB gene product	U14003	<i>Escherichia coli</i>	306	48
ORF547	597755	598612	ORF-2	D11024	<i>Shigella flexneri</i>	168	46
ORF548	598602	599204	homologous to DNA glycosylases; hypothetical	D83026	<i>Bacillus subtilis</i>	374	47
ORF549	599373	599939	putative				
ORF550	600903	602072	hemolysin	X73141	<i>Serpulina hyodysenteriae</i>	362	36
ORF551	602240	602587	hypothetical protein	D90908	<i>Synechocystis sp.</i>	182	35
ORF552	602637	603272	putative				
ORF553	603142	604512	putative				
ORF554	604627	605853	conserved hypothetical protein	AE000579	<i>Helicobacter pylori</i>	423	40
ORF555	605790	606620	putative				
ORF556	606571	607281	putative	L14679	<i>Lactococcus lactis</i>	384	45
ORF557	609004	607355	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF558	610906	609932	putative				
ORF559	611786	611004	diaminopimelate epimerase	D90917	<i>Synechocystis sp.</i>	207	55
ORF560	612333	611746	ATP-dependent Clp protease proteolytic subunit	D90915	<i>Synechocystis sp.</i>	389	44
ORF561	613897	612341	serine hydroxymethyltransferase	D90903	<i>Synechocystis sp.</i>	909	52
ORF562	615179	616279	putative				
ORF563	616610	617383	putative				
ORF564	618796	617810	ORF o328	U18997	<i>Escherichia coli</i>	413	45
ORF565	620004	618826	branched chain alpha-keto acid dehydrogenase E2	M97391	<i>Bacillus subtilis</i>	688	41
ORF566	619649	619918	putative				
ORF567	621265	620021	Hypothetical protein	Y14083	<i>Bacillus subtilis</i>	727	37
ORF568	622359	621265	hypothetical	U32691	<i>Haemophilus influenzae</i>	294	52
ORF569	623420	622560	rRNA methylase	D90913	<i>Synechocystis sp.</i>	244	38
ORF570	624297	623335	hypothetical protein (SP:P39587)	U67605	<i>Meihamococcus jannaschii</i>	147	35
ORF571	624773	624174	riboflavin synthase alpha chain	AE000261	<i>Escherichia coli</i>	424	50
ORF572	625029	625484	ORF 168	D28752	<i>Synechococcus sp.</i>	323	43
ORF573	625488	625883	YteA	AF008220	<i>Bacillus subtilis</i>	172	35
ORF574	625892	626395	signalpeptidase II	X78084	<i>Staphylococcus carnosus</i>	204	38
ORF575	626444	627790	D-alanine permease (dagA)	U32770	<i>Haemophilus influenzae</i>	566	33
ORF576	627912	628607	putative				
ORF577	628774	629697	putative				
ORF578	629660	631639	POMP91A	U65942	<i>Chlamydia psittaci</i>	579	44
ORF579	631725	633551	putative				
ORF580	633520	636957	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	266	45
ORF581	637232	638098	adhesion protein	D90903	<i>Synechocystis sp.</i>	267	38
ORF582	640648	639593	GTP-binding protein	D90901	<i>Synechocystis sp.</i>	759	45
ORF583	640979	640728	50S ribosomal protein L27	U38804	<i>Porphyra purpurea</i>	265	65
ORF584	641327	641007	50S ribosomal subunit protein L21	U18997	<i>Escherichia coli</i>	210	41
ORF585	641687	642283	hypothetical protein	D90906	<i>Synechocystis sp.</i>	76	39
ORF586	643023	642286	assimilatory sulfite reductase	L26503	<i>Saccharomyces cerevisiae</i>	284	42
ORF587	643330	643076	putative				
ORF588	643704	643351	ribosomal protein S10 (rpS10)	U32761	<i>Haemophilus influenzae</i>	349	69

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF589	645628	643676	translation elongation factor EF-G (fusa)	AE000625	<i>Helicobacter pylori</i>	1991	58
ORF590	645783	645538	elongation factor G (AA 1-691)	X16278	<i>Thermus aquaticus thermophilus</i>	170	80
ORF591	646269	645793	ribosomal protein S7	Z11567	<i>Chlamydia trachomatis</i>	730	88
ORF592	646751	646314	ribosomal protein S12 (AA 1-123)	X52912	<i>Cryptomonas phi</i>	485	67
ORF593	647848	647045	putative				
ORF594	648393	650336	ORF of prc gene (alt.)	D00674	<i>Escherichia coli</i>	554	42
ORF595	651016	650420	hypothetical sulfur-rich protein	U41759	<i>Chlamydia psittaci</i>	301	50
ORF596	652956	651289	60kDa CrP	X53511	<i>Chlamydia pneumoniae</i>	2951	100
ORF597	653395	653126	9kDa CrP	X53511	<i>Chlamydia pneumoniae</i>	502	99
ORF598	655740	654193	glutamyl-tRNA synthetase homolog	U41759	<i>Chlamydia psittaci</i>	2259	82
ORF599	656508	655966	early stage-specific transcription experimentally demonstrated; early upstream open reading frame (EUO)	L13598	<i>Chlamydia psittaci</i>	666	62
ORF600	658140	657022	unknown	U41759	<i>Chlamydia psittaci</i>	950	44
ORF601	660216	658525	RecJ recombination protein	U41759	<i>Chlamydia psittaci</i>	807	73
ORF602	663238	660248	protein-export membrane protein SecD	D64000	<i>Synechocystis sp.</i>	413	41
ORF603	664461	663157	putative				
ORF604	665735	664635	putative				
ORF605	666212	666994	hypothetical protein	D64006	<i>Synechocystis sp.</i>	538	58
ORF606	666998	667921	o298; This 298 aa orf is 33 pct identical (24 gaps) to 248 residues of an approx. 256 aa protein CDSA_ECOLI SW: P06466	AE000238	<i>Escherichia coli</i>	253	45
ORF607	667909	668568	cytidylate kinase	AE000193	<i>Escherichia coli</i>	400	48
ORF608	668502	669203	hypothetical protein	D90915	<i>Synechocystis sp.</i>	225	33
ORF609	669154	670893	arginyl-tRNA-synthetase	D64006	<i>Synechocystis sp.</i>	1365	49
ORF610	672226	670853	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	U32788	<i>Haemophilus influenzae</i>	642	40
ORF611	671137	671424	putative				
ORF612	672453	673001	putative				
ORF613	673072	674721	putative				
ORF614	674549	674262	putative				
ORF615	675518	674796	ORF246 gene product	X59551	<i>Escherichia coli</i>	520	43
ORF616	676083	675499	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF617	676630	676067	putative				
ORF618	677016	676600	ORF3	D10279	<i>Bacillus subtilis</i>	361	63
ORF619	677647	677015	peptide release factor 2	X99401	<i>Bacillus firmus</i>	427	43
ORF620	677990	678259	unknown	Z49939	<i>Saccharomyces cerevisiae</i>	175	48
ORF621	679444	680097	unknown	D26185	<i>Bacillus subtilis</i>	263	38
ORF622	680097	680897	unknown	D64126	<i>Bacillus subtilis</i>	506	45
ORF623	681637	680849	putative				
ORF624	681409	682281	putative				
ORF625	682453	682821	putative				
ORF626	682763	683902	sensor protein	L39904	<i>Myxococcus xanthus</i>	190	48
ORF627	684616	683969	putative				
ORF628	685169	684534	putative				
ORF629	685986	685117	putative				
ORF630	686278	687288	NtrC/NifA-like protein regulator	U17902	<i>Escherichia coli</i>	820	45
ORF631	687483	688151	putative				
ORF632	688740	689501	putative				
ORF633	690242	689622	putative				
ORF634	690470	691126	unknown	Z48008	<i>Saccharomyces cerevisiae</i>	380	46
ORF635	692600	691497	putative				
ORF636	692674	695064	phenylalanyl-tRNA synthetase beta-subunit (pheT)	U32810	<i>Haemophilus influenzae</i>	593	45
ORF637	695049	696032	putative				
ORF638	697964	696585	OppC-like protein	D85103	<i>Synechococcus sp.</i>	371	37
ORF639	699803	698274	OppB gene product	X56347	<i>Bacillus subtilis</i>	197	40
ORF640	701926	699788	AppA	U20909	<i>Bacillus subtilis</i>	324	43
ORF641	703196	702567	putative				
ORF642	704221	703208	putative				
ORF643	704240	705289	ferrochelatase	X73417	<i>Arabidopsis thaliana</i>	266	42
ORF644	706070	705300	histidine periplasmic binding protein P29	U58045	<i>Campylobacter jejuni</i>	128	31
ORF645	706841	706254	conserved hypothetical protein	AE000592	<i>Helicobacter pylori</i>	155	37
ORF646	707596	706811	putative				
ORF647	708666	707677	ADP-glucose pyrophosphorylase	X55650	<i>Solanum tuberosum</i>	595	43
ORF648	709793	709119	pyrE-F gene product	X71842	<i>Arabidopsis thaliana</i>	400	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF649	711523	710132	transcription termination factor	J01673	<i>Escherichia coli</i>	1251	60
ORF650	712236	711523	putative				
ORF651	714734	712125	DNA polymerase I	J04479	<i>Streptococcus pneumoniae</i>	1334	43
ORF652	715759	714761	protease IV	U67512	<i>Methanococcus jannaschii</i>	101	55
ORF653	717538	715886	adenine nucleotide translocase	Z49227	<i>Arabidopsis thaliana</i>	832	39
ORF654	719113	720243	replicative DNA helicase	D26185	<i>Bacillus subtilis</i>	776	44
ORF655	720590	722422	homologous to E.coli gidA	X62540	<i>Pseudomonas putida</i>	1575	52
ORF656	722406	723056	putative				
ORF657	723551	723120	nucleoside 5'-diphosphate phosphotransferase (EC 2.7.4.6)	J05207	<i>Myxococcus xanthus</i>	451	62
ORF658	724246	723626	Holliday junction DNA helicase (ruvA)	U32716	<i>Haemophilus influenzae</i>	293	43
ORF659	724754	724251	crossover junction endodeoxyribonuclease (ruvC)	U32717	<i>Haemophilus influenzae</i>	296	53
ORF660	725868	724900	putative				
ORF661	727115	726270	putative				
ORF662	728126	727119	glyceraldehyde-3-phosphate dehydrogenase	U83198	<i>Chlamydia trachomatis</i>	1340	75
ORF663	728594	728208	ribosomal protein L17	L33834	<i>Chlamydia trachomatis</i>	439	82
ORF664	729614	728604	RNA polymerase alpha-subunit	L33834	<i>Chlamydia trachomatis</i>	1356	89
ORF665	729778	729533	RNA polymerase alpha-subunit	L33834	<i>Chlamydia trachomatis</i>	273	82
ORF666	730149	729751	ribosomal protein S11	L33834	<i>Chlamydia trachomatis</i>	562	90
ORF667	730539	730174	ribosomal protein S13	L33834	<i>Chlamydia trachomatis</i>	544	89
ORF668	731983	730598	homolog	L25077	<i>Chlamydia trachomatis</i>	1956	83
ORF669	732427	731996	ribosomal protein CtrL15e	M80325	<i>Chlamydia trachomatis</i>	563	77
ORF670	732917	732423	ribosomal protein CtrS5e	M80325	<i>Chlamydia trachomatis</i>	702	84
ORF671	733598	733320	ribosomal protein L6	M60652	<i>Chlamydia trachomatis</i>	316	87
ORF672	733869	733492	ribosomal protein L6	M60652	<i>Chlamydia trachomatis</i>	469	77
ORF673	734298	733900	ribosomal protein CtrS8e	M80325	<i>Chlamydia trachomatis</i>	572	82
ORF674	734858	734319	ribosomal protein CtrL5e	M80325	<i>Chlamydia trachomatis</i>	730	90
ORF675	735195	734863	ribosomal protein CtrL24e	M80325	<i>Chlamydia trachomatis</i>	420	70
ORF676	735578	735342	ribosomal protein CtrL14e	M80325	<i>Chlamydia trachomatis</i>	270	95
ORF677	735861	735604	ribosomal protein S17e	M80325	<i>Chlamydia trachomatis</i>	322	77
ORF678	736492	736079	50S ribosomal protein L16	D90905	<i>Synechocystis sp.</i>	439	60

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF679	737192	736524	ribosomal protein S3	D64071	<i>Actinobacillus actinomycetemcomitans</i>	612	58
ORF680	737555	737211	ribosomal protein L22	Z21677	<i>Thermotoga maritima</i>	228	48
ORF681	738688	737837	50S ribosomal subunit protein L2	U18997	<i>Escherichia coli</i>	769	62
ORF682	739048	738713	putative				
ORF683	739736	739065	ribosomal protein L4	X67014	<i>Bacillus stearothermophilus</i>	308	46
ORF684	740477	739773	ribosomal protein L3	Z46265	<i>Thermus aquaticus thermophilus</i>	463	50
ORF685	740659	740958	putative				
ORF686	741722	740721	putative				
ORF687	742789	741827	methionyl-tRNA formyltransferase	D64001	<i>Synechocystis sp.</i>	511	48
ORF688	743618	742782	UDP-N-acetylglucosamine acyltransferase	L22690	<i>Rickettsia rickettsii</i>	542	43
ORF689	744092	743634	(3R)-hydroxymyristol acyl carrier protein dehydrase	D90910	<i>Synechocystis sp.</i>	339	55
ORF690	744604	744107	UDP-3-O-acyl N-acetylglucosamine deacetylase	D90902	<i>Synechocystis sp.</i>	287	45
ORF691	744953	744498	UDP-3-O-acyl-GlcNAc deacetylase	U67855	<i>Pseudomonas aeruginosa</i>	262	51
ORF692	746608	744986	apolipoprotein N-acyltransferase (cute)	U32716	<i>Haemophilus influenzae</i>	194	50
ORF693	747085	746621	low homology to P14 protein of Hemophilus influenzae and 14.2 kDa protein of Escherichia coli	D78189	<i>Bacillus subtilis</i>	235	37
ORF694	747974	747219	polymerase III	M22996	<i>Bacillus subtilis</i>	180	34
ORF695	748594	748169	hypothetical protein	D90914	<i>Synechocystis sp.</i>	160	43
ORF696	749145	748573	putative				
ORF697	749652	749957	trxA	L39892	<i>Chlamydia psittaci</i>	393	72
ORF698	750446	749979	spoU	L39892	<i>Chlamydia psittaci</i>	559	72
ORF699	751219	750446	mip	L39892	<i>Chlamydia psittaci</i>	948	60
ORF700	753042	751291	aspartyl-tRNA synthetase	D90910	<i>Synechocystis sp.</i>	1347	47
ORF701	754309	753020	histidine--tRNA ligase	Z17214	<i>Sreptococcus equisimilis</i>	757	44
ORF702	755120	756175	hexosephosphate transport protein	M89480	<i>Salmonella typhimurium</i>	870	49
ORF703	756120	756485	hexosephosphate transport protein	M89479	<i>Escherichia coli</i>	321	45
ORF704	756499	760227	DNA polymerase III alpha-subunit (dnaE)	AE000646	<i>Helicobacter pylori</i>	1977	42
ORF705	761217	760297	putative				
ORF706	761297	761809	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF707	761782	762282	putative				
ORF708	762260	762895	putative				
ORF709	762867	763316	hypothetical protein	D90908	<i>Synechocystis sp.</i>	177	43
ORF710	763780	763325	putative				
ORF711	763861	765168	DD-carboxypeptidase	M85047	<i>Bacillus subtilis</i>	292	37
ORF712	766809	765697	fmu and fmv protein	D90902	<i>Synechocystis sp.</i>	130	36
ORF713	768051	766888	putative				
ORF714	768566	768321	putative				
ORF715	769342	768551	putative				
ORF716	770532	769378	putative				
ORF717	771451	770804	putative				
ORF718	773058	771847	3-phosphoglycerate kinase	U83197	<i>Chlamydia trachomatis</i>	1540	72
ORF719	773094	773456	putative				
ORF720	774376	773093	putative phosphate permease	U84890	<i>Mesembryanthemum crystallinum</i>	870	45
ORF721	775123	774380	putative				
ORF722	775398	774916	putative				
ORF723	775046	776077	sporulation protein	M57689	<i>Bacillus subtilis</i>	698	43
ORF724	776070	777041	was dppE	U00039	<i>Escherichia coli</i>	565	56
ORF725	777964	777536	orf288; translated orf similarity to SWISS-PROT: YGI2_PSEPU hypothetical 32.4 kDa protein of <i>Pseudomonas putida</i>	Y10436	<i>Coxiella burnetii</i>	256	46
ORF726	778176	777904	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB	X62539	<i>Bacillus subtilis</i>	112	37
ORF727	778621	779334	putative				
ORF728	781173	780307	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA SCHPO SW: O10089	AE000263	<i>Escherichia coli</i>	603	40
ORF729	781526	781116	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA SCHPO SW: O10089	AE000263	<i>Escherichia coli</i>	258	45
ORF730	782784	781555	f423; This 423 aa orf is 29 pct identical (1 gaps) to 172 residues of an approx. 488 aa protein YC24 CYAPA SW: P48260	AE000263	<i>Escherichia coli</i>	197	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF731	783572	782805	hypothetical chloroplast ORF 16	U38804	<i>Porphyra purpurea</i>	597	52
ORF732	785032	783581	ABC transporter subunit	D64004	<i>Synechocystis sp.</i>	1720	62
ORF733	786412	785360	putative				
ORF734	788429	786450	pbp	Y14206	<i>Streptomyces coelicolor</i>	148	55
ORF735	788944	788528	penicillin-binding protein 3	X84053	<i>Pseudomonas aeruginosa</i>	148	38
ORF736	789758	788901	putative				
ORF737	790332	791504	major outer membrane protein	M64064	<i>Chlamydia pneumoniae</i>	2028	99
ORF738	791846	792721	ribosomal protein S2	U60196	<i>Chlamydia trachomatis</i>	904	70
ORF739	792724	793569	elongation factor Ts	U60196	<i>Chlamydia trachomatis</i>	1023	71
ORF740	793580	794323	UMP kinase	U60196	<i>Chlamydia trachomatis</i>	891	72
ORF741	794304	794843	ribosome-releasing factor	U60196	<i>Chlamydia trachomatis</i>	673	73
ORF742	795217	795732	unknown	D26185	<i>Bacillus subtilis</i>	105	42
ORF743	795722	796795	unknown	D26185	<i>Bacillus subtilis</i>	208	33
ORF744	798735	797053	putative	L33796	<i>Vibrio cholerae</i>	386	34
ORF745	799823	798681	putative				
ORF746	799297	799578	putative				
ORF747	801313	799808	Plk5	U40656	<i>Myxococcus xanthus</i>	345	33
ORF748	802453	801332	putative				
ORF749	803299	802457	putative				
ORF750	803811	803290	putative				
ORF751	805151	803826	YscN	U02499	<i>Yersinia enterocolitica</i>	1185	53
ORF752	805860	805156	putative				
ORF753	806604	806332	putative				
ORF754	806913	806608	putative				
ORF755	808222	806903	putative				
ORF756	808751	808146	putative				
ORF757	809437	808673	putative				
ORF758	809939	809454	putative				
ORF759	811235	810213	delta-aminolevulinatase synthase (EC 2.3.1.37)	M30785	<i>Escherichia coli</i>	172	40
ORF760	811779	813056	DNA gyrase subunit B	U35453	<i>Clostridium acetobutylicum</i>	584	38
ORF761	812890	812516	putative				
ORF762	812954	813583	DNA gyrase subunit B	Z19108	<i>Spiroplasma citri</i>	371	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF763	813587	815023	gyrA	X92503	<i>Mycobacterium smegmatis</i>	414	55
ORF764	815420	815746	putative				
ORF765	816036	817010	orf-X; hypothetical protein; Method: conceptual translation supplied by author	U48870	<i>Bacillus subtilis</i>	569	47
ORF766	817111	817356	unknown	Z74024	<i>Mycobacterium tuberculosis</i>	114	34
ORF767	817791	818609	3-deoxy-d-manno-octulosonic acid 8- phosphate synthetase	Z50747	<i>Chlamydia psittaci</i>	1112	78
ORF768	818609	819094	protein of unknown function	Z50747	<i>Chlamydia psittaci</i>	545	65
ORF769	819104	819823	ATP binding protein	U72493	<i>Chlamydia trachomatis</i>	1099	88
ORF770	820722	819826	putative				
ORF771	822313	821000	putative				
ORF772	823503	822238	putative				
ORF773	823678	825612	putative				
ORF774	825461	826312	putative				
ORF775	827280	826645	putative				
ORF776	828604	827171	76 kDa protein	L23921	<i>Chlamydia pneumoniae</i>	2179	100
ORF777	830026	828713	76 kDa protein	L23921	<i>Chlamydia pneumoniae</i>	1162	100
ORF778	831047	830085	mvIB homolog	U50732	<i>Chlamydia trachomatis</i>	982	58
ORF779	831725	831051	mvIB homolog	U50732	<i>Chlamydia trachomatis</i>	740	65
ORF780	832220	833098	T05H10.2	Z47812	<i>Caenorhabditis elegans</i>	407	34
ORF781	833851	833396	ribosomal protein S4 (rps4)	AE000633	<i>Helicobacter pylori</i>	372	53
ORF782	834068	835039	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from <i>E. coli</i> . Accession Number X61000	L22217	<i>Mycoplasma-like organism</i>	377	49
ORF783	835792	835127	uridine kinase	L31783	<i>Mus musculus</i>	436	43
ORF784	837624	836116	ORF f397	U29581	<i>Escherichia coli</i>	92	38
ORF785	838951	840882	putative				
ORF786	840869	842185	exodeoxyribonuclease V (recB)	U32811	<i>Haemophilus influenzae</i>	409	40
ORF787	841989	843455	DNA helicase II	U39703	<i>Mycoplasma genitalium</i>	110	46
ORF788	843242	844021	exodeoxyribonuclease V (recB)	U32811	<i>Haemophilus influenzae</i>	196	40
ORF789	845018	843987	MreC protein	M31792	<i>Escherichia coli</i>	76	53
ORF790	846174	844990	aspartate aminotransferase (aspC)	X03629	<i>Escherichia coli</i>	754	40
ORF791	848509	846311	GreA	U02878	<i>Rickettsia prowazekii</i>	190	35

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF792	848568	849014	putative				
ORF793	849082	850488	NADH:ubiquinone oxidoreductase subunit A (GP:Z37111_2)	U32702	<i>Haemophilus influenzae</i>	445	37
ORF794	851512	850574	porphobilinogen synthase	U38348	<i>Chlorobium vibrioforme</i>	769	45
ORF795	852064	852447	putative				
ORF796	852398	853690	putative				
ORF797	855118	854243	geranylgeranyl pyrophosphate synthase	D85029	<i>Arabidopsis thaliana</i>	408	41
ORF798	855751	855128	f147; This 147 aa orf is 26 pct identical (1 gaps) to 99 residues of an approx. 728 aa protein E2BE RABIT SW: P47823	AE000143	<i>Escherichia coli</i>	187	36
ORF799	856551	855829	membrane associated regulatory protein	M28368	<i>Salmonella typhimurium</i>	172	36
ORF800	856730	858556	unknown function	Z32530	<i>Chlamydia trachomatis</i>	842	35
ORF801	858717	859601	exodeoxyribonuclease V (recD)	U32811	<i>Haemophilus influenzae</i>	182	51
ORF802	859591	860205	exonuclease V alpha subunit (AA 1-608)	X04582	<i>Escherichia coli</i>	235	45
ORF803	861132	860284	putative				
ORF804	861426	861163	30S ribosomal protein S20	Z67753	<i>Odontella sinensis</i>	153	41
ORF805	861701	862921	putative				
ORF806	863026	864798	major sigma factor	U04442	<i>Chlamydia psittaci</i>	2661	94
ORF807	864831	865256	putative				
ORF808	865226	866581	dihydropterin pyrophosphokinase /dihydropteroate synthase	Y08611	<i>Pisum sativum</i>	455	48
ORF809	866562	867119	dehydrofolate reductase, type I (folA)	U32772	<i>Haemophilus influenzae</i>	213	49
ORF810	867025	867816	M. jannaschii predicted coding region MJ0768	U67522	<i>Methanococcus jannaschii</i>	207	36
ORF811	867820	868497	putative				
ORF812	869743	868661	RecA	U16739	<i>Chlamydia trachomatis</i>	1512	87
ORF813	870633	870094	unknown function	Z32530	<i>Chlamydia trachomatis</i>	308	45
ORF814	871929	870646	unknown function	Z32530	<i>Chlamydia trachomatis</i>	1410	63
ORF815	872538	872086	putative				
ORF816	873908	872517	putative				
ORF817	874281	874670	nifR3-like gene product	Z37984	<i>Azospirillum brasilense</i>	181	32
ORF818	874582	875286	ORF1 gene product	X62399	<i>Escherichia coli</i>	307	42
ORF819	877857	875377	DNA topoisomerase I	L27797	<i>Bacillus subtilis</i>	1488	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF820	878446	879255	putative				
ORF821	880635	879268	sigma factor (ntrA) (AA 1-502)	X05888	<i>Azotobacter vinelandii</i>	257	47
ORF822	882524	880593	DNA helicase II	D90906	<i>Synechocystis</i> sp.	1140	50
ORF823	882612	883319	ipa-57d gene product	X73124	<i>Bacillus subtilis</i>	601	51
ORF824	884155	883538	hypothetical protein	D90915	<i>Synechocystis</i> sp.	344	39
ORF825	884340	885611	19/20 residue stretch (32-51) identical to N-terminal putative signal sequence of unknown, partly cloned <i>B. subtilis</i> gene.;	L19954	<i>Bacillus subtilis</i>	456	37
ORF826	885722	887302	putative				
ORF827	887587	888153	heat shock protein	L12004	<i>Chlamydia trachomatis</i>	915	39
ORF828	888627	888220	basI protein	Z34917	<i>Hordeum vulgare</i>	474	50
ORF829	889330	888716	putative				
ORF830	889898	889323	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	223	55
ORF831	891190	889898	peptidoglycan-associated lipoprotein	X65796	<i>Escherichia coli</i>	222	50
ORF832	891828	891247	TolB	U32470	<i>Haemophilus influenzae</i>	280	35
ORF833	892421	892017	putative				
ORF834	893116	892421	exbD peptide	M28819	<i>Escherichia coli</i>	77	48
ORF835	892521	892925	inner membrane protein (tolQ)	U32722	<i>Haemophilus influenzae</i>	157	54
ORF836	893392	895419	putative				
ORF837	895745	896527	inner membrane copper tolerance protein	Z36905	<i>Escherichia coli</i>	120	35
ORF838	896668	897558	unknown	D26185	<i>Bacillus subtilis</i>	381	41
ORF839	897565	899442	succinate dehydrogenase subunit C	Y08563	<i>Paenibacillus macerans</i>	253	40
ORF840	899420	900229	succinate dehydrogenase subunit A	Y08563	<i>Paenibacillus macerans</i>	1667	57
ORF841	903230	900237	succinate dehydrogenase subunit B	Y08563	<i>Paenibacillus macerans</i>	656	54
ORF842	905081	903234	putative				
ORF843	906931	905045	putative				
ORF844	907248	907832	sigma factor SibG regulation protein RsbU	D90905	<i>Synechocystis</i> sp.	117	35
ORF845	907784	908128	putative				
ORF846	908132	908677	putative				
ORF847	908589	909320	putative				
ORF848	909405	911465	putative				
ORF849	911677	912360	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF850	912303	912821	putative				
ORF851	912937	913983	putative				
ORF852	915128	914067	putative				
ORF853	916658	915303	enolase	L29475	<i>Bacillus subtilis</i>	1036	60
ORF854	915627	915376	enolase	U43738	<i>Mycoplasma pneumoniae</i>	226	65
ORF855	917707	916853	excinuclease ABC subunit B (uvrB)	U32804	<i>Haemophilus influenzae</i>	724	46
ORF856	918837	917722	excinuclease ABC subunit B (uvrB)	U32804	<i>Haemophilus influenzae</i>	1029	54
ORF857	919868	918837	tryptophanyl-tRNA synthetase (trpS)	U32746	<i>Haemophilus influenzae</i>	376	40
ORF858	920434	919880	putative				
ORF859	921187	920438	ORF8	X82078	<i>Chlamydia sp.</i>	164	50
ORF860	921959	921195	hypothetical protein	X62475	<i>Chlamydia psittaci</i>	511	44
ORF861	923773	921995	Threonyl tRNA Synthetase	Z80360	<i>Bacillus subtilis</i>	1476	44
ORF862	922146	922415	putative				
ORF863	923943	923674	putative				
ORF864	924077	925006	putative				
ORF865	925436	925083	putative				
ORF866	926524	925349	putative				
ORF867	927920	926433	putative				
ORF868	928319	927951	putative				
ORF869	928963	928334	putative				
ORF870	929248	930987	DNA mismatch repair protein (mutL)	U32692	<i>Haemophilus influenzae</i>	585	40
ORF871	930995	932059	YqhT	D84432	<i>Bacillus subtilis</i>	445	39
ORF872	932121	933515	putative				
ORF873	932881	932513	putative				
ORF874	933485	935746	pulD (ttg start codon)	M32613	<i>Klebsiella pneumoniae</i>	210	33
ORF875	935724	937082	epsE	M96172	<i>Vibrio cholerae</i>	890	55
ORF876	937229	938410	PilG	U32588	<i>Neisseria gonorrhoeae</i>	280	38
ORF877	938281	938805	putative				
ORF878	938809	939255	putative				
ORF879	939165	939782	putative				
ORF880	939760	940791	putative				
ORF881	940822	941106	putative				
ORF882	940977	941351	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF883	942537	941623	yscT	L25667	<i>Yersinia pseudotuberculosis</i>	169	44
ORF884	942784	942500	yscS	L25667	<i>Yersinia pseudotuberculosis</i>	173	42
ORF885	943149	942799	HcrR	AE000107	<i>Rhizobium sp. NGR234</i>	265	52
ORF886	943799	943029	pathogenicity protein	M64094	<i>Xanthomonas campestris</i>	252	41
ORF887	944055	943732	putative	M74011	<i>Yersinia enterocolitica</i>	112	33
ORF888	944413	943994	putative				
ORF889	945395	944556	putative				
ORF890	945853	945389	putative				
ORF891	946392	945751	HcrJ	U56662	<i>Erwinia amylovora</i>	229	44
ORF892	947410	948081	putative				
ORF893	949871	948915	ORF YOR196c	Z75104	<i>Saccharomyces cerevisiae</i>	702	44
ORF894	951058	949868	dihydrolipoamide dehydrogenase E3 subunit	M57435	<i>Bacillus subtilis</i>	745	39
ORF895	951249	950959	dihydrolipoamide acetyltransferase E3 subunit	M73535	<i>Staphylococcus aureus</i>	166	49
ORF896	951664	952134	putative				
ORF897	952674	952165	SNF	X98455	<i>Bacillus cereus</i>	229	47
ORF898	953491	952589	helicase	U39680	<i>Mycoplasma genitalium</i>	307	42
ORF899	955324	953495	F01G4.1	Z68341	<i>Caenorhabditis elegans</i>	133	57
ORF900	955823	955281	putative				
ORF901	957082	955847	branched-chain amino acid carrier	Z48676	<i>Lactobacillus delbrueckii</i>	297	40
ORF902	957902	957270	endonuclease III	U11289	<i>Bacillus subtilis</i>	317	37
ORF903	959231	957906	homologous to E.coli 50K	X62539	<i>Bacillus subtilis</i>	805	45
ORF904	959376	960284	phosphatidylserine decarboxylase	U72715	<i>Chlamydia trachomatis</i>	776	51
ORF905	960266	961669	putative				
ORF906	961856	964765	secretory component	U06928	<i>Caulobacter crescentus</i>	1812	55
ORF907	966855	965395	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative	L47648	<i>Bacillus subtilis</i>	778	41
ORF908	968204	966975	poly(A) polymerase	L47709	<i>Bacillus subtilis</i>	383	41
ORF909	968791	968237	ClpX-like protein	U18229	<i>Bacillus subtilis</i>	340	39
ORF910	969498	968731	ATP-dependent protease ATPase subunit	D64006	<i>Synechocystis sp.</i>	846	66
ORF911	969858	969511	ClpP	U16135	<i>Synechococcus sp.</i>	257	54

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF912	970118	969762	ATP-dependent clp protease proteolytic component (clpP)	AE000591	<i>Helicobacter pylori</i>	362	63
ORF913	970593	970300	putative				
ORF914	971261	970542	putative				
ORF915	971680	971123	putative				
ORF916	971876	975100	SNF				
ORF917	975419	976516	MreB protein	X98455	<i>Bacillus cereus</i>	778	49
ORF918	976584	978320	phospho enol pyruvate carboxykinase	M96343	<i>Bacillus subtilis</i>	960	55
ORF919	977680	977231	putative	S56812	<i>Chlorobium limicola</i>	1667	64
ORF920	978399	980738	putative				
ORF921	980756	981928	putative				
ORF922	982974	981931	precursor protein (AA -22 to 371)	X52557	<i>Chlamydia trachomatis</i>	97	50
ORF923	984120	983119	NAD+ dependent glycerol-3-phosphate dehydrogenase	L47648	<i>Bacillus subtilis</i>	618	43
ORF924	985502	984120	AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa]	S73498	<i>Homo sapiens</i>	254	34
ORF925	987180	985882	ORF 4	M72718	<i>Bacillus subtilis</i>	697	38
ORF926	987172	987444	putative				
ORF927	989846	989049	niU-like protein	AE000542	<i>Helicobacter pylori</i>	302	31
ORF928	991048	989846	putative				
ORF929	991638	990955	phosphoglyceromutase				
ORF930	991794	992498	ORFX13	L09651	<i>Zymomonas mobilis</i>	471	53
ORF931	993619	993041	biotin [acetyl-CoA-carboxylase] ligase	L09228	<i>Bacillus subtilis</i>	403	39
ORF932	993530	994792	rod-shape-determining protein	L47709	<i>Bacillus subtilis</i>	136	38
ORF933	995970	994795	cadmium-transporting ATPase	M22857	<i>Escherichia coli</i>	312	44
ORF934	996857	995739	ATPase	D64005	<i>Synechocystis sp.</i>	358	47
ORF935	997603	996782	putative	L28104	<i>Transposon Tn5422</i>	449	39
ORF936	998969	997572	seryl-trna synthetase	Y09924	<i>Staphylococcus aureus</i>	851	42
ORF937	998896	1000023	orf2, homologue to B.subtilis ribG	X64395	<i>Escherichia coli</i>	596	40
ORF938	1000087	1001340	GTP cyclohydrolase II	D90912	<i>Synechocystis sp.</i>	1078	52
ORF939	1001357	1001818	riboflavin synthase beta subunit	U27202	<i>Actinobacillus pleuropneumoniae</i>	278	36
ORF940	1003288	1001873	putative				
ORF941	1003487	1004146	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF942	1004485	1005639	D-alanine glycine permease (dagA)	AE000603	<i>Helicobacter pylori</i>	394	33
ORF943	1005643	1005972	hypothetical protein MTCY180.08	Z97193	<i>Mycobacterium tuberculosis</i>	274	58
ORF944	1006784	1006116	similar to trithorax protein in final three exons	U13875	<i>Caenorhabditis elegans</i>	155	46
ORF945	1007563	1006769	yycJ	D78193	<i>Bacillus subtilis</i>	406	38
ORF946	1009226	1007568	YtpT	AF008220	<i>Bacillus subtilis</i>	992	47
ORF947	1009989	1009336	putative				
ORF948	1015852	1016337	putative				
ORF949	1016561	1016181	putative				
ORF950	1016297	1017532	putative				
ORF951	1016802	1016452	putative				
ORF952	1018993	1017701	phenolhydroxylase component	U32702	<i>Haemophilus influenzae</i>	909	47
ORF953	1019454	1019137	ORF	M63939	<i>Escherichia coli</i>	96	45
ORF954	1020764	1019562	pCTHom1 gene product	M94254	<i>Chlamydia trachomatis</i>	1185	65
ORF955	1021405	1021037	histone H1-like protein	M80324	<i>Chlamydia psittaci</i>	319	62
ORF956	1021821	1024286	phosphoprotein	L25078	<i>Chlamydia trachomatis</i>	739	41
ORF957	1024697	1024248	putative				
ORF958	1025569	1024508	protoporphyrinogen oxidase	U25114	<i>Mus musculus</i>	86	38
ORF959	1026969	1025590	oxygen independent coprophorphyrinogen III oxidase	D90912	<i>Synechocystis sp.</i>	880	42
ORF960	1027789	1026947	uroporphyrinogen decarboxylase	M97208	<i>Bacillus subtilis</i>	372	38
ORF961	1031199	1027945	transcription-repair coupling factor (trcF) (mfd)	U32805	<i>Haemophilus influenzae</i>	1584	42
ORF962	1031717	1031172	alanyl-tRNA synthetase	X95571	<i>Thiobacillus ferrooxidans</i>	76	31
ORF963	1033057	1031612	alanyl-tRNA synthetase	AE000353	<i>Escherichia coli</i>	889	40
ORF964	1033425	1033039	alanyl-tRNA synthetase (alaS)	AE000629	<i>Helicobacter pylori</i>	327	51
ORF965	1033784	1033200	alanyl-tRNA synthetase	X59956	<i>Rhizobium leguminosarum</i>	416	47
ORF966	1033963	1036038	transketolase	Z73234	<i>Bacillus subtilis</i>	1398	44
ORF967	1036945	1036010	AMP nucleosidase	AE000290	<i>Escherichia coli</i>	265	42
ORF968	1037110	1037679	elongation factor P	U14003	<i>Escherichia coli</i>	458	51
ORF969	1037696	1037944	putative				
ORF970	1038916	1037975	putative				
ORF971	1040582	1039026	HSP60 chaperonin	X62914	<i>Clostridium perfringens</i>	284	31

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF972	1040997	1042337	PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15)	AB001488	<i>Bacillus subtilis</i>	446	39
ORF973	1042357	1043403	ORF-Y (AA 1-360)	X51584	<i>Escherichia coli</i>	582	45
ORF974	1043367	1044623	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	U32793	<i>Haemophilus influenzae</i>	348	42
ORF975	1044607	1045362	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	115	38
ORF976	1045384	1046538	spoVE gene product (AA 1-366)	X51419	<i>Bacillus subtilis</i>	479	35
ORF977	1046447	1047517	mur	Y13922	<i>Enterococcus hirae</i>	256	45
ORF978	1047521	1049956	UDP-N-acetylmuramate-alanine ligase (murC)	U32794	<i>Haemophilus influenzae</i>	756	38
ORF979	1050611	1050036	unknown	Z74024	<i>Mycobacterium tuberculosis</i>	78	44
ORF980	1050925	1050566	cycY gene product	U14003	<i>Escherichia coli</i>	179	34
ORF981	1051728	1051090	putative				
ORF982	1051743	1052063	hypothetical protein	D90908	<i>Synechocystis</i> sp.	135	33
ORF983	1052101	1053126	trna delta(2)-isopentenylpyrophosphate transferase	Z98209	<i>Mycobacterium tuberculosis</i>	441	37
ORF984	1054201	1053107	conserved hypothetical protein	AE000579	<i>Helicobacter pylori</i>	826	44
ORF985	1054242	1055555	putative				
ORF986	1055483	1055908	putative				
ORF987	1056609	1056965	YqeL	D84432	<i>Bacillus subtilis</i>	202	38
ORF988	1056961	1058232	beta-ketoacyl-ACP synthase	L13242	<i>Ricinus communis</i>	1266	55
ORF989	1058238	1058687	diadenosine tetraphosphatase	U30313	<i>Homo sapiens</i>	122	42
ORF990	1059371	1058727	inorganic pyrophosphatase (ppa)	AE000576	<i>Helicobacter pylori</i>	209	39
ORF991	1059526	1060578	leucine dehydrogenase LeuDH	U51099	<i>Bacillus cereus</i>	680	45
ORF992	1061553	1060579	3'(2'),5'-bisphosphate nucleotidase	U40433	<i>Arabidopsis thaliana</i>	335	43
ORF993	1061674	1062411	putative				
ORF994	1062377	1064077	2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase	U29581	<i>Escherichia coli</i>	383	44
ORF995	1064116	1065243	7-keto-8-aminopelargonic acid synthetase (bioF)	M29291	<i>Bacillus sphaericus</i>	200	35
ORF996	1067451	1065178	priA	Y10304	<i>Bacillus subtilis</i>	1009	43

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF997	1068065	1067376	putative				
ORF998	1068209	1068706	putative				
ORF999	1069958	1068819	unknown	U41759	<i>Chlamydia psittaci</i>	777	41
ORF1000	1071163	1070033	unknown	U41759	<i>Chlamydia psittaci</i>	381	36
ORF1001	1072438	1071332	unknown	U41759	<i>Chlamydia psittaci</i>	254	37
ORF1002	1072997	1073476	putative				
ORF1003	1074239	1075864	lysyl-tRNA synthetase	D90906	<i>Synechocystis sp.</i>	1007	48
ORF1004	1076790	1075867	cysteinyI-tRNA synthetase	L14580	<i>Bacillus subtilis</i>	395	52
ORF1005	1077268	1076573	cys-tRNA synthetase (cysS)	U32693	<i>Haemophilus influenzae</i>	431	56
ORF1006	1077999	1078724	putative				
ORF1007	1079088	1078672	ribonuclease P protein component (gtg start codon)	M11056	<i>Escherichia coli</i>	78	46
ORF1008	1079642	1079944	30S ribosomal subunit protein S14	U18997	<i>Escherichia coli</i>	260	50
ORF1009	1080501	1079995	F18C12.2	Z75536	<i>Caenorhabditis elegans</i>	118	38
ORF1010	1080775	1081341	putative				
ORF1011	1083158	1081350	deoxyribodipyrimidine photolyase	J03294	<i>Bacillus subtilis</i>	687	44
ORF1012	1084677	1083235	DNA mismatch repair protein	U71154	<i>Aquifex pyrophilus</i>	735	48
ORF1013	1085648	1084632	DNA mismatch repair protein	D90909	<i>Synechocystis sp.</i>	565	39
ORF1014	1086117	1086737	DNA primase (dnaG)	U32735	<i>Haemophilus influenzae</i>	303	40
ORF1015	1086692	1087897	DnaG	Z83860	<i>Mycobacterium tuberculosis</i>	222	37
ORF1016	1088646	1089005	putative				
ORF1017	1089146	1089805	putative				
ORF1018	1092931	1089890	glycyl-tRNA synthetase	U20547	<i>Chlamydia trachomatis</i>	2569	48
ORF1019	1093179	1092889	putative				
ORF1020	1093584	1094204	phosphatidylglycerophosphate synthase	U87792	<i>Bacillus subtilis</i>	163	55
ORF1021	1095619	1094192	glycogen (starch) synthase	D90899	<i>Synechocystis sp.</i>	574	40
ORF1022	1096074	1096628	partial ctc gene product (AA 1-186)	X16518	<i>Bacillus subtilis</i>	86	37
ORF1023	1096633	1097082	peptidyl-tRNA hydrolase	U31570	<i>Chlamydia trachomatis</i>	378	53
ORF1024	1097266	1097601	ribosomal protein S6 (rps6)	AE000630	<i>Helicobacter pylori</i>	179	39
ORF1025	1097622	1097867	ribosomal protein S18 homolog; putative	M62820	<i>Chlamydia trachomatis</i>	324	86
ORF1026	1097886	1098392	putative heat shock protein ORF; putative	M62820	<i>Chlamydia trachomatis</i>	190	79
ORF1027	1099521	1099279	putative				
ORF1028	1099689	1101053	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1029	1102192	1101107	putative				
ORF1030	1104950	1102116	glycerol-3-phosphate acyltransferase	M80571	<i>Cucumis sativus</i>	574	43
ORF1031	1106508	1104946	ORF_f495; orf of ECMRED, uses 2nd start	U18997	<i>Escherichia coli</i>	855	38
ORF1032	1106722	1107249	putative				
ORF1033	1107463	1108101	PlsX	U59433	<i>Bacillus subtilis</i>	282	45
ORF1034	1108041	1108421	fatty acid/phospholipid synthesis protein (plsX)	AE000540	<i>Helicobacter pylori</i>	205	35
ORF1035	1108520	1113370	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	352	44
ORF1036	1114958	1113447	putative				
ORF1037	1116915	1115071	lipid A disaccharide synthetase (lpxB)	U32786	<i>Haemophilus influenzae</i>	477	42
ORF1038	1118183	1116894	poly(A) polymerase	AE000123	<i>Escherichia coli</i>	555	46
ORF1039	1118846	1120030	putative	L12968	<i>Escherichia coli</i>	880	50
ORF1040	1120040	1120522	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	AE000651	<i>Helicobacter pylori</i>	396	52
ORF1041	1120510	1121430	glutamine amidotransferase; glucosamine--fructose-6-phosphate aminotransferase	AE000450	<i>Escherichia coli</i>	494	44
ORF1042	1121321	1121866	L-glutamine:D-fructose-6-P	U17352	<i>Thermus aquaticus thermophilus</i>	374	50
ORF1043	1122123	1122899	amidotransferase precursor	AE000284	<i>Escherichia coli</i>	281	41
ORF1044	1124842	1125564	tyrosine-specific transport protein				
ORF1045	1126526	1125579	putative	U32760	<i>Haemophilus influenzae</i>	497	41
ORF1046	1126519	1127676	cell division protein (ftsY)	J01619	<i>Escherichia coli</i>	784	43
ORF1047	1127672	1128571	succinyl-CoA synthetase beta-subunit	U23408	<i>Dictyostelium discoideum</i>	978	63
ORF1048	1130230	1131336	succinyl coenzyme A synthetase alpha subunit				
ORF1049	1131480	1132553	putative				
ORF1050	1132830	1133843	putative				
ORF1051	1134121	1134855	serine protease HtrA	D90905	<i>Synechocystis sp.</i>	307	51
ORF1052	1134642	1135592	GsrA protein	D78376	<i>Yersinia enterocolitica</i>	497	41
ORF1053	1135964	1135653	putative				
ORF1054	1137132	1135954	R11H6.1	Z93386	<i>Caenorhabditis elegans</i>	445	37
ORF1055	1137169	1140102	Ydr430cp; CAI: 0.15	U33007	<i>Saccharomyces cerevisiae</i>	559	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1056	1141365	1140112	hypothetical 54.7 kD protein in udp 3' region precursor (o475)	AE000459	<i>Escherichia coli</i>	222	34
ORF1057	1142150	1141356	phosphatidylserine synthase (pssA)	AE000614	<i>Helicobacter pylori</i>	307	41
ORF1058	1142520	1145660	ribonucleotide reductase subunit M1	K02927	<i>Mus musculus</i>	1433	45
ORF1059	1145627	1146721	ribonucleoside diphosphate reductase, beta subunit (nrdB)	AE000553	<i>Helicobacter pylori</i>	443	32
ORF1060	1146862	1147545	unknown	Z95398	<i>Mycobacterium leprae</i>	191	35
ORF1061	1147666	1148190	YtqB	AF008220	<i>Bacillus subtilis</i>	262	44
ORF1062	1148514	1148224	ORF2	U01958	<i>Bacillus licheniformis</i>	135	54
ORF1063	1149136	1148348	ORF2	M31827	<i>Bacillus subtilis</i>	268	40
ORF1064	1149702	1149166	putative				
ORF1065	1150031	1150591	unknown	Z85982	<i>Mycobacterium tuberculosis</i>	445	49
ORF1066	1150785	1151147	ribosomal protein L20 (AA 1-119)	X16188	<i>Bacillus stearothermophilus</i>	273	44
ORF1067	1151165	1152181	phenylalanyl-tRNA synthetase beta subunit	Z75208	<i>Bacillus subtilis</i>	777	40
ORF1068	1152522	1154591	putative				
ORF1069	1155666	1154566	putative				
ORF1070	1156743	1155670	putative				
ORF1071	1156859	1157815	hypothetical	U32723	<i>Haemophilus influenzae</i>	252	42
ORF1072	1157982	1160735	ATP-binding protein	U01376	<i>Escherichia coli</i>	1314	56
ORF1073	1162620	1160917	polynucleotide phosphorylase	AF010578	<i>Pisum sativum</i>	1416	52
ORF1074	1162970	1162590	polynucleotide phosphorylase	U52048	<i>Spinacia oleracea</i>	312	53
ORF1075	1163532	1164020	orf150 gene product	X95938	<i>Porphyromonas gingivalis</i>	335	43
ORF1076	1163995	1164294	putative				
ORF1077	1165569	1165030	putative				
ORF1078	1166108	1165566	putative				
ORF1079	1166644	1166141	putative				
ORF1080	1167055	1168374	putative				
ORF1081	1169218	1168337	methionine aminopeptidase	D64003	<i>Synechocystis sp.</i>	488	54
ORF1082	1169823	1169218	ORF o197	U18997	<i>Escherichia coli</i>	281	30
ORF1083	1171324	1170572	putative				
ORF1084	1172085	1171177	hypothetical	U32720	<i>Haemophilus influenzae</i>	162	44
ORF1085	1172394	1173773	fumarase	D64000	<i>Synechocystis sp.</i>	1292	57
ORF1086	1175209	1173881	prs-associated putative membrane protein	U02424	<i>Escherichia coli</i>	570	39

ORF	Begin	End	Homology	ID	Species	Score	%
ORF1087	1175555	1175127	hypothetical protein in pth-prs intergenic region	AE000219	<i>Escherichia coli</i>	278	46
ORF1088	1175778	1177043	hypothetical protein	Z96072	<i>Mycobacterium tuberculosis</i>	109	43
ORF1089	1177177	1179048	putative				
ORF1090	1179156	1180085	penicillin tolerance protein (lytB)	U32781	<i>Haemophilus influenzae</i>	731	54
ORF1091	1180045	1180779	putative				
ORF1092	1181942	1180788	putative				
ORF1093	1182296	1181961	putative				
ORF1094	1183844	1182300	putative				
ORF1095	1184420	1183848	putative				
ORF1096	1185382	1184366	putative				
ORF1097	1185858	1185226	putative				
ORF1098	1186164	1186481	putative				
ORF1099	1187386	1186484	site-specific recombinase	U92524	<i>Salmonella typhimurium</i>	401	48
ORF1100	1187370	1189028	phosphoglucosyltransferase-like protein	L40822	<i>Chlamydia trachomatis</i>	1154	63
ORF1101	1189321	1190889	putative				
ORF1102	1191142	1192146	NADP-malate dehydrogenase	L40958	<i>Flavobacterium bidentis</i>	775	46
ORF1103	1191974	1191729	putative				
ORF1104	1193815	1192991	putative				
ORF1105	1195702	1194248	o460; This 460 aa orf is 46 pct identical (26 gaps) to 458 residues of an approx. 488 aa protein ARCD_PSEAE SW: P18275	AE000256	<i>Escherichia coli</i>	1022	44
ORF1106	1196303	1195716	putative				
ORF1107	1196831	1196337	putative				
ORF1108	1197807	1196746	putative				
ORF1109	1198740	1197883	putative				
ORF1110	1200232	1198721	shikimate 5-dehydrogenase	U67551	<i>Methanococcus jannaschii</i>	245	37
ORF1111	1201286	1200135	3-dehydroquinate synthase (aroB)	U32705	<i>Haemophilus influenzae</i>	478	45
ORF1112	1202386	1201259	2,3-dihydroxybenzoic acid	L29562	<i>Vibrio anguillarum</i>	780	50
ORF1113	1202901	1202350	putative				
ORF1114	1204162	1202816	5-enolpyruvylshikimate 3-phosphate synthase	U67500	<i>Methanococcus jannaschii</i>	520	40
ORF1115	1203177	1203464	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1116	1205028	1204180	putative				
ORF1117	1206392	1204878	bioA gene product	A02587	unidentified	834	48
ORF1118	1206742	1206086	dethiobiotin synthase (bioD)	U32830	<i>Haemophilus influenzae</i>	243	37
ORF1119	1207872	1206724	L-alanine - pimelyl CoA ligase	U51868	<i>Bacillus subtilis</i>	601	41
ORF1120	1208852	1207851	biotin synthase	U24147	<i>Arabidopsis thaliana</i>	892	52
ORF1121	1210518	1209742	tryptophan hydroxylase	U26428	<i>Gallus gallus</i>	237	34
ORF1122	1210703	1211494	dihydrodipicolinate reductase	U47017	<i>Pseudomonas syringae pv. tabaci</i>	345	37
ORF1123	1211870	1212754	aspartate-semialdehyde dehydrogenase	U67476	<i>Methanococcus jannaschii</i>	444	43
ORF1124	1212742	1214064	aspartokinase III	U00006	<i>Escherichia coli</i>	473	47
ORF1125	1214046	1214858	dihydrodipicolinate synthase	D64006	<i>Synechocystis sp.</i>	238	40
ORF1126	1215551	1216318	putative				
ORF1127	1216493	1216849	putative				
ORF1128	1217183	1219612	putative				
ORF1129	1220068	1219673	putative				
ORF1130	1219710	1220669	putative				
ORF1131	1220630	1221376	putative				
ORF1132	1221645	1223681	unknown	D26185	<i>Bacillus subtilis</i>	621	43
ORF1133	1223894	1224988	putative				
ORF1134	1225000	1225830	high level kasgamyacin resistance	D26185	<i>Bacillus subtilis</i>	422	41
ORF1135	1227810	1225879	hypothetical protein	D90903	<i>Synechocystis sp.</i>	1129	43
ORF1136	1226528	1226908	putative				
ORF1137	1229972	1228311	exonuclease VII, large subunit (xseA)	U32723	<i>Haemophilus influenzae</i>	666	46
ORF1138	47569	47018	Integrase/recombinase	AE001308	<i>Chlamydia trachomatis</i>	716	72
ORF1139	49980	49117	putative				
ORF1140	53356	52898	putative				
ORF1141	54477	54884	O-Sialoglycoprotein Endopeptidase	AE001307	<i>Chlamydia trachomatis</i>	311	51
ORF1142	63753	63998	PTS PEP Phosphotransferase	AE001306	<i>Chlamydia trachomatis</i>	198	61
ORF1143	77164	77487	putative				
ORF1144	79724	79302	Sms Protein	AE001302	<i>Chlamydia trachomatis</i>	458	57
ORF1145	88721	88951	putative				
ORF1146	94067	94429	putative				
ORF1147	122832	123341	hypothetical protein	AE001303	<i>Chlamydia trachomatis</i>	398	61
ORF1148	147536	147234	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1149	158990	159346	S16 Ribosomal Protein	AE001277	<i>Chlamydia trachomatis</i>	467	78
ORF1150	168470	168979	putative				
ORF1151	169183	169452	putative				
ORF1152	171785	171504	Cationic Amino Acid Transporter	AE001278	<i>Chlamydia trachomatis</i>	262	68
ORF1153	172518	171775	Cationic Amino Acid Transporter	AE001278	<i>Chlamydia trachomatis</i>	533	48
ORF1154	193599	194045	putative				
ORF1155	195704	196075	S/T Protein Kinase	AE001288	<i>Chlamydia trachomatis</i>	536	82
ORF1156	210687	210145	KDO-transferase	X80061	<i>Chlamydia pneumoniae</i>	856	96
ORF1157	211100	210708	putative				
ORF1158	215420	215088	putative				
ORF1159	217914	218246	putative				
ORF1160	218925	218701	putative				
ORF1161	223785	223525	IMP dehydrogenase	U13372	<i>Borrelia burgdorferi</i>	270	63
ORF1162	224271	223999	putative				
ORF1163	228691	228407	putative				
ORF1164	235050	235334	(Methylase)	AE001287	<i>Chlamydia trachomatis</i>	331	66
ORF1165	252308	253021	Oligopeptide Permease	AE001293	<i>Chlamydia trachomatis</i>	838	72
ORF1166	258280	258912	Dicarboxylate Translocator	AE001294	<i>Chlamydia trachomatis</i>	909	80
ORF1167	261325	261567	putative				
ORF1168	268195	268878	hypothetical protein	AE001287	<i>Chlamydia trachomatis</i>	556	52
ORF1169	269447	268881	putative				
ORF1170	271263	271538	putative				
ORF1171	271957	272346	putative				
ORF1172	274176	274550	putative				
ORF1173	275736	275314	Disulfide bond Oxidoreductase	AE001291	<i>Chlamydia trachomatis</i>	519	73
ORF1174	276490	276927	hypothetical protein	AE001291	<i>Chlamydia trachomatis</i>	249	53
ORF1175	277577	277861	hypothetical protein	AE001291	<i>Chlamydia trachomatis</i>	256	52
ORF1176	288163	287909	putative				
ORF1177	290130	289789	putative				
ORF1178	290989	291225	putative				
ORF1179	291372	291860	adenylate cyclase	AE001286	<i>Chlamydia trachomatis</i>	388	48
ORF1180	311239	311622	putative				
ORF1181	328665	328384	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1182	337348	338289	sodium-dependent transporter	AF017105	<i>Chlamydia psittaci</i>	1112	72
ORF1183	364764	364369	Prolipoprotein Diacylglycerol Transferase	AE001298	<i>Chlamydia trachomatis</i>	300	54
ORF1184	389623	390135	hypothetical protein	AE001282	<i>Chlamydia trachomatis</i>	75	33
ORF1185	393729	394343	ABC superfamily ATPase	AE001282	<i>Chlamydia trachomatis</i>	473	52
ORF1186	407379	407621	putative				
ORF1187	410944	410708	putative				
ORF1188	427632	427988	putative				
ORF1189	428172	428486	putative				
ORF1190	436761	437246	hypothetical protein	AE001279	<i>Chlamydia trachomatis</i>	661	81
ORF1191	460911	461159	putative				
ORF1192	477597	477313	hypothetical protein	AE001300	<i>Chlamydia trachomatis</i>	309	62
ORF1193	487303	487001	putative				
ORF1194	487764	487534	Glycine Cleavage System H Protein	AE001300	<i>Chlamydia trachomatis</i>	221	67
ORF1195	498502	499017	hypothetical protein	AE001275	<i>Chlamydia trachomatis</i>	206	32
ORF1196	499795	500466	putative				
ORF1197	571928	572344	putative				
ORF1198	572367	572131	putative				
ORF1199	588184	587915	hypothetical protein	AE001312	<i>Chlamydia trachomatis</i>	256	62
ORF1200	600587	600907	(Metalloenzyme)	AE001316	<i>Chlamydia trachomatis</i>	314	61
ORF1201	609731	608895	putative				
ORF1202	614039	614755	hypothetical protein	AE001317	<i>Chlamydia trachomatis</i>	475	46
ORF1203	614823	615152	putative				
ORF1204	638244	638831	ABC Transporter ATPase	AE001315	<i>Chlamydia trachomatis</i>	614	61
ORF1205	638819	639094	(Metal Transport Protein)	AE001315	<i>Chlamydia trachomatis</i>	265	63
ORF1206	639073	639636	(Metal Transport Protein)	AE001315	<i>Chlamydia trachomatis</i>	687	69
ORF1207	647901	648236	hypothetical protein	AE001317	<i>Chlamydia trachomatis</i>	139	38
ORF1208	678510	679469	phosphohydrolase	AE001320	<i>Chlamydia trachomatis</i>	995	63
ORF1209	688178	688732	hypothetical protein	AE001320	<i>Chlamydia trachomatis</i>	366	43
ORF1210	696045	696563	methyltransferase	AE001321	<i>Chlamydia trachomatis</i>	369	49
ORF1211	708998	708588	Glucose-1-P Adenylyltransferase	AE001322	<i>Chlamydia trachomatis</i>	507	83
ORF1212	709808	710089	putative				
ORF1213	718240	717737	Glycerol-3-P Phosphatidyltransferase	AE001323	<i>Chlamydia trachomatis</i>	573	66
ORF1214	737828	737565	S19 Ribosomal Protein	AE001323	<i>Chlamydia trachomatis</i>	439	94

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1215	779502	780257	hypothetical protein	AE001322	<i>Chlamydia trachomatis</i>	476	48
ORF1216	806310	805864	hypothetical protein	AE001337	<i>Chlamydia trachomatis</i>	512	67
ORF1217	820931	820707	putative				
ORF1218	837696	839096	Exodeoxyribonuclease V, Gamma	AE001334	<i>Chlamydia trachomatis</i>	967	49
ORF1219	883307	883549	putative				
ORF1220	892010	891726	putative				
ORF1221	893277	893564	putative				
ORF1222	936998	937225	Gen. Secretion Protein E	AE001327	<i>Chlamydia trachomatis</i>	256	67
ORF1223	946865	947419	putative				
ORF1224	975187	975411	SWF/SNF family helicase	AE001341	<i>Chlamydia trachomatis</i>	363	96
ORF1225	985882	985517	hypothetical protein	AE001342	<i>Chlamydia trachomatis</i>	166	33
ORF1226	987713	987180	hypothetical protein	AE001342	<i>Chlamydia trachomatis</i>	447	59
ORF1227	988215	987733	Flagellar M-Ring Protein	AE001342	<i>Chlamydia trachomatis</i>	304	44
ORF1228	988754	988530	Flagellar M-Ring Protein	AE001342	<i>Chlamydia trachomatis</i>	92	36
ORF1229	992542	992841	hypothetical protein	AE001343	<i>Chlamydia trachomatis</i>	112	39
ORF1230	992759	993067	hypothetical protein	AE001343	<i>Chlamydia trachomatis</i>	100	32
ORF1231	1004247	1004528	D-Ala/Gly Permease	AE001344	<i>Chlamydia trachomatis</i>	283	64
ORF1232	1015013	1014294	235aa long hypothetical protein	AB009472	<i>Pyrococcus horikoshii</i>	104	54
ORF1233	1056147	1056545	putative				
ORF1234	1077682	1078035	predicted disulfide bond isomerase	AE001351	<i>Chlamydia trachomatis</i>	233	46
ORF1235	1088121	1088381	putative				
ORF1236	1098430	1098852	Predicted Kinase	AE001352	<i>Chlamydia trachomatis</i>	384	59
ORF1237	1098798	1099319	Predicted Kinase	AE001352	<i>Chlamydia trachomatis</i>	322	45
ORF1238	1123198	1123515	Transport Permease	AE001354	<i>Chlamydia trachomatis</i>	313	72
ORF1239	1123606	1124256	Tyrosine Transport	AE001354	<i>Chlamydia trachomatis</i>	577	58
ORF1240	1124453	1124797	Tyrosine Transport	AE001354	<i>Chlamydia trachomatis</i>	323	50
ORF1241	1129253	1129567	putative				
ORF1242	1164947	1164474	hypothetical protein	AE001357	<i>Chlamydia trachomatis</i>	412	56
ORF1243	1170457	1170053	hypothetical protein	AE001358	<i>Chlamydia trachomatis</i>	283	59
ORF1244	1172342	1171863	ABC transporter permease	AE001358	<i>Chlamydia trachomatis</i>	457	55
ORF1245	1192155	1192835	putative				
ORF1246	1192759	1192992	putative				
ORF1247	1193861	1194142	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1248	1194036	1193779	(D-Amino Acid Dehydrogenase)	AE001311	<i>Chlamydia trachomatis</i>	269	79
ORF1249	1209748	1209053	conserved hypothetical protein	AE000958	<i>Archaeoglobus fulgidus</i>	121	38
ORF1250	1215111	1215419	putative				
ORF1251	1216302	1216538	putative				
ORF1252	1228072	1227818	hypothetical protein	AE001306	<i>Chlamydia trachomatis</i>	134	39
ORF1253	1228304	1228080	xseB	AL021897	<i>Mycobacterium tuberculosis</i>	89	33
ORF1254	26599	26222	putative				
ORF1255	27609	27367	putative				
ORF1256	67206	66967	putative				
ORF1257	70612	70352	putative				
ORF1258	132703	132945	putative				
ORF1259	178073	178393	putative				
ORF1260	208576	208349	putative				
ORF1261	209156	208929	putative				
ORF1262	209263	209024	putative				
ORF1263	210304	210639	putative				
ORF1264	299009	299452	putative				
ORF1265	352106	351717	putative				
ORF1266	420182	419949	Flagellar Secretion Protein	AE001280	<i>Chlamydia trachomatis</i>	115	43
ORF1267	553602	553381	putative				
ORF1268	556538	556807	putative				
ORF1269	594348	593797	putative				
ORF1270	595169	594876	putative				
ORF1271	662148	662381	putative				
ORF1272	706528	706893	putative				
ORF1273	803315	803650	putative				
ORF1274	849551	849306	putative				
ORF1275	913676	913275	putative				
ORF1276	927087	926836	putative				
ORF1277	930587	930360	putative				
ORF1278	986531	986764	ORF 12	M72718	<i>Bacillus subtilis</i>	106	48
ORF1279	996229	996486	putative				
ORF1280	1000373	1000002	putative				

ORF	Begin	End	Homology	ID	Species	Score	1%
ORF1281	1010291	1010037	putative				
ORF1282	1011128	1010793	106aa long hypothetical protein	AB009472	<i>Pyrococcus horikoshii</i>	159	50
ORF1283	1012924	1012694	putative				
ORF1284	1028659	1028913	putative				
ORF1285	1086481	1086762	putative				
ORF1286	1118658	1118879	Phosphoglucomutase	AE001354	<i>Chlamydia trachomatis</i>	291	84
ORF1287	1170098	1169835	hypothetical protein	AE001358	<i>Chlamydia trachomatis</i>	187	53
ORF1288	1180828	1181184	putative				
ORF1289	1182658	1183035	putative				
ORF1290	1195076	1194795	putative				
ORF1291	1195890	1196183	putative				

Table 2

ORF Nos	begin	end	potential start
2	42	794	42
3	1258	1614	1261
4	1807	2418	1807
5	3393	2491	3393
6	3639	4067	3639
7	5649	4270	5649
8	7463	6012	7463
9	8051	8962	8051
10	9129	9959	9138
11	10687	10361	10639
12	10927	11232	10927
13	11246	12727	11246
14	12691	14190	12691
15	14484	17249	14484
16	16039	15770	16036
17	17845	20853	17845
18	21137	22042	21137
19	22046	23476	22046
20	23681	26110	23681
21	26109	25861	26109
22	26241	26978	26241
23	26960	27754	26960
24	27747	28577	27747
25	28887	29492	28950
26	29432	30028	29432
27	30024	31472	30024
28	31758	32288	31758
29	32201	33991	32201
30	33852	34541	33852
31	34783	36063	34783
32	36009	37529	36009
33	37881	39362	37881
34	39418	39161	39418

ORF Nos	begin	end	potential start
35	39366	40715	39366
36	43076	41094	43076
37	43800	43066	43800
38	44828	43785	44768
39	45340	44753	45340
40	45752	45372	45752
41	46996	45701	46996
42	47961	47569	47961
43	48960	48040	48960
44	51452	50133	51452
45	52606	51335	52606
46	53684	53319	53684
47	54195	53746	54195
48	55278	56453	55278
49	56493	57266	56493
50	57297	58526	57297
51	59851	58565	59851
52	61495	59924	61495
53	61324	62151	61324
54	62132	62470	62132
55	62474	63733	62474
56	63881	64186	63881
57	64611	64318	64611
58	65485	64673	65485
59	65999	65301	65999
60	66244	67281	66244
61	67265	67699	67265
62	67703	68539	67760
63	68805	70736	68805
64	69172	68831	69172
65	70642	71142	70642
66	71325	72029	71325
67	72060	73637	72060
68	74061	76175	74061

ORF Nos	begin	end	potential start
69	78351	77680	78351
70	79356	78355	79356
71	79983	79693	79983
72	80441	79938	80441
73	80475	80969	80475
74	81296	83080	81332
75	83291	83932	83291
76	84005	84769	84005
77	84975	85244	84975
78	85123	85425	85123
79	85397	85903	85397
80	85909	86583	85909
81	86626	88065	86626
82	89257	91026	89257
83	91291	93030	91291
84	93295	94086	93295
85	95285	94707	95279
86	95667	96557	95667
87	96317	97456	96317
88	98435	97968	98435
89	99460	98426	99460
90	100144	101325	100144
91	101457	101720	101457
92	101704	102273	101704
93	102356	102805	102356
94	102835	103530	102835
95	103549	104058	103549
96	104096	104491	104096
97	104601	108386	104601
98	108401	112054	108401
99	112033	112590	112033
100	112672	113682	112672
101	113726	114121	113726
102	114711	114136	114711

ORF Nos	begin	end	potential start
103	115267	115755	115267
104	115911	116543	115911
105	116736	118055	116778
106	117968	118522	117968
107	118530	119843	118530
108	119816	120457	119816
109	120451	122430	120451
110	122504	122950	122504
111	123528	126347	123528
112	126332	129166	126332
113	134690	129213	134690
114	134925	136382	134931
115	137870	136482	137867
116	137899	138240	137899
117	138239	137928	138239
118	139558	138257	139558
119	140352	139516	140352
120	140498	141841	140498
121	141855	142658	141855
122	144258	143050	144258
123	145258	144494	145258
124	145454	146749	145454
125	147318	146767	147318
126	148261	147677	148261
127	149029	152157	149029
128	154108	152201	154108
129	155135	154308	155135
130	155141	155467	155141
131	155703	156779	155703
132	156748	157635	156748
133	157653	158996	157653
134	159363	159986	159363
135	159880	160446	159880
136	160477	160839	160477

ORF Nos	begin	end	potential start
137	160898	161539	160898
138	161527	162153	161527
139	162144	162443	162144
140	162437	164098	162437
141	165451	164228	165451
142	166349	165411	166349
143	166949	168442	166949
144	169416	171029	169416
145	170857	171459	170857
146	172652	173428	172652
147	174626	173439	174626
148	174816	175613	174816
149	175598	175954	175598
150	175958	176935	175958
151	177708	176938	177708
152	177128	177376	177128
153	179472	177841	179472
154	179822	179517	179822
155	181793	179943	181793
156	182628	181876	182628
157	184420	183074	184420
158	184988	184467	184988
159	185483	185112	185483
160	185902	185483	185902
161	186174	185839	186174
162	187720	186587	187720
163	188318	190933	188318
164	191090	191635	191090
165	191547	192743	191547
166	192969	193469	192969
167	194044	193610	194044
168	194196	195809	194196
169	196088	198073	196088
170	198132	199454	198132

ORF Nos	begin	end	potential start
171	199351	202818	199351
172	204552	202999	204552
173	205648	204692	205639
174	205807	207327	205807
175	207182	207775	207182
176	207779	208267	207779
177	208267	209577	208267
178	211807	211271	211807
179	212188	211844	212188
180	214079	212448	214079
181	214907	214083	214907
182	216154	215429	216154
183	216115	216678	216115
184	216728	217282	216728
185	217267	217866	217267
186	218593	218261	218590
187	219821	218994	219821
188	221382	220309	221382
189	222719	221433	222719
190	223521	222724	223521
191	224499	225008	224499
192	225140	225559	225140
193	225555	226802	225555
194	227800	226892	227743
195	228335	228072	228335
196	229251	228643	229251
197	230983	229622	230983
198	231483	230983	231483
199	232063	231509	232063
200	232739	232053	232739
201	233166	234356	233166
202	233518	233165	233518
203	234536	235186	234536
204	235379	236689	235379

ORF Nos	begin	end	potential start
205	236680	237618	236689
206	237521	238345	237521
207	238281	238973	238281
208	238871	240115	238871
209	240191	241564	240191
210	242281	241604	242281
211	242933	242274	242933
212	243416	242976	243416
213	243500	244531	243500
214	244480	246021	244480
215	246330	247811	246330
216	247831	249174	247870
217	249437	251038	249455
218	251325	252212	251325
219	253156	254007	253156
220	253974	254852	253974
221	255258	256094	255258
222	256640	257455	256640
223	257502	258239	257502
224	257869	257501	257869
225	259248	260897	259248
226	262753	261788	262753
227	263059	262757	263059
228	264375	263182	264375
229	265985	264747	265985
230	266637	266059	266637
231	267338	266538	267338
232	267922	267473	267922
233	269647	270771	269647
234	272777	273145	272777
235	273253	273636	273253
236	273705	273977	273705
237	276016	275717	276016
238	276439	276020	276418

ORF Nos	begin	end	potential start
239	276792	277253	276792
240	277318	277599	277318
241	278578	277877	278578
242	279258	278554	279258
243	280435	279533	280435
244	281547	280849	281547
245	281696	282325	281717
246	282459	284069	282459
247	284056	284517	284056
248	284606	285775	284606
249	285592	285987	285592
250	286179	286976	286179
251	287583	287002	287583
252	287951	287451	287951
253	288499	288816	288499
254	289674	288505	289674
255	288839	289213	288839
256	289970	290254	289970
257	291931	292803	291931
258	293258	292755	293258
259	293718	293272	293718
260	294630	293953	294630
261	296153	294636	296153
262	294817	295068	294817
263	296354	297862	296354
264	298415	297879	298415
265	298777	298253	298777
266	299572	298781	299572
267	300487	299633	300487
268	301586	300702	301568
269	302440	301571	302440
270	302838	302437	302838
271	303335	302745	303335
272	304394	303852	304394

ORF Nos	begin	end	potential start
273	304606	305223	304606
274	305394	306236	305394
275	306501	307439	306501
276	308033	307458	308033
277	308924	308037	308924
278	309485	310180	309485
279	310426	311214	310426
280	311597	311253	311504
281	312772	311780	312772
282	313425	312772	313425
283	313646	313377	313646
284	313937	314665	313937
285	315576	314755	315576
286	316157	315531	316157
287	318657	316156	318657
288	321042	318676	321042
289	321445	321098	321445
290	322309	321710	322309
291	323190	322366	323181
292	323843	323181	323843
293	324878	323856	324878
294	325340	326410	325340
295	326433	327836	326433
296	328465	327839	328465
297	329360	328857	329360
298	330907	329357	330907
299	332455	330956	332455
300	334536	332395	334536
301	336091	334877	336091
302	336103	337302	336103
303	338129	338830	338129
304	338965	339501	338965
305	339508	340143	339508
306	340247	342967	340247

ORF Nos	begin	end	potential start
307	343385	343810	343385
308	344171	343935	344171
309	345082	344330	345073
310	346005	345082	346005
311	346784	346437	346784
312	347029	346715	347029
313	347034	347723	347034
314	348075	350459	348075
315	350598	351071	350598
316	351075	352175	351096
317	353291	352230	353267
318	353442	354467	353442
319	354451	354933	354451
320	355000	355449	355000
321	355448	356743	355448
322	355953	355642	355953
323	359310	356827	359310
324	359120	359377	359120
325	359525	359908	359525
326	361290	359947	361290
327	363785	361362	363746
328	364496	363888	364496
329	364832	365290	364832
330	365304	365669	365304
331	366599	365667	366599
332	367291	369030	367291
333	369134	369808	369134
334	369917	370438	369917
335	370365	372647	370365
336	372557	373066	372557
337	373020	373442	373020
338	373467	374195	373467
339	374176	375099	374176
340	375676	375083	375676

ORF Nos	begin	end	potential start
341	376173	375634	376173
342	376564	377643	376564
343	377956	379773	377956
344	379781	380425	379805
345	380281	381000	380281
346	381008	381460	381008
347	381460	383037	381460
348	383257	383523	383257
349	383553	385304	383553
350	385397	386458	385400
351	387242	386514	387242
352	388764	387013	388764
353	390120	390932	390120
354	390919	391818	390961
355	392379	391885	392379
356	392582	392986	392582
357	392776	393684	392776
358	394151	394804	394151
359	394928	395308	394928
360	395259	395990	395259
361	397815	395953	397815
362	398850	397831	398850
363	400085	399099	400085
364	401245	400073	401236
365	401474	401136	401474
366	402199	401423	402199
367	403193	402186	403166
368	403650	404165	403650
369	404343	405914	404343
370	405984	407327	405984
371	407712	408806	407712
372	410439	409075	410439
373	411826	410954	411826
374	412482	414302	412482

ORF Nos	begin	end	potential start
375	415402	414407	415402
376	415848	415237	415848
377	417131	415866	417131
378	417258	417566	417258
379	418326	417454	418326
380	420057	418426	420057
381	420448	420720	420448
382	420980	421552	420980
383	421556	422029	421556
384	422461	422925	422461
385	423562	424320	423562
386	424250	424591	424250
387	424830	426047	424830
388	426240	427397	426240
389	428841	430703	428841
390	430694	431446	430694
391	431597	432100	431597
392	432165	432779	432165
393	433272	432832	433272
394	433925	433227	433922
395	436678	433934	436678
396	437176	438357	437176
397	440317	438518	440317
398	440001	440345	440001
399	441233	440517	441233
400	440719	441012	440719
401	442192	441230	442192
402	442888	442343	442888
403	442371	442961	442371
404	443578	443003	443578
405	444500	443526	444500
406	444842	444528	444842
407	445009	444743	445009
408	445718	445182	445718

ORF Nos	begin	end	potential start
409	445807	447804	445807
410	448738	447803	448738
411	449628	448618	449628
412	450298	450867	450298
413	450713	451207	450713
414	451211	452452	451211
415	452448	453659	452448
416	454843	453725	454843
417	455608	454865	455608
418	456243	457007	456243
419	457016	457708	457016
420	458368	457979	458368
421	459496	458372	459496
422	459493	460194	459493
423	461446	460355	461446
424	462298	461450	462298
425	462444	463349	462444
426	464241	463342	464241
427	464574	465065	464574
428	465129	465611	465129
429	465571	466317	465571
430	466317	467093	466317
431	466999	467502	466999
432	469691	467715	469691
433	470691	469660	470691
434	472010	470709	472010
435	471545	471799	471545
436	472359	472045	472359
437	473523	472732	473523
438	474889	473441	474889
439	477323	475365	477323
440	478496	477597	478496
441	478722	479273	478722
442	479277	479705	479277

ORF Nos	begin	end	potential start
443	480050	481450	480050
444	481469	482053	481469
445	482600	482025	482600
446	482654	484204	482654
447	484211	485170	484211
448	485170	485838	485170
449	485813	486580	485813
450	486976	486638	486976
451	489071	487764	489071
452	489341	489090	489341
453	489958	489152	489958
454	490549	489962	490549
455	491163	490522	491163
456	491396	491112	491396
457	492121	491390	492121
458	492304	494838	492304
459	495943	494822	495943
460	496011	496565	496170
461	496569	497228	496569
462	497358	497834	497358
463	497770	498327	497770
464	499209	499589	499209
465	499520	499792	499520
466	500774	504169	500774
467	504139	504600	504139
468	504865	506877	504865
469	506790	507671	506790
470	507718	510507	507718
471	508325	507912	508325
472	510660	513440	510660
473	514965	513787	514920
474	517347	515419	517347
475	517058	517363	517058
476	517798	517277	517798

ORF Nos	begin	end	potential start
477	518200	517847	518200
478	518300	521146	518363
479	521392	522948	521407
480	523244	524809	523322
481	524379	524125	524379
482	524649	526238	524649
483	526265	527104	526268
484	526947	526702	526947
485	526975	528450	526975
486	528408	529199	528408
487	530612	529542	530612
488	531656	530616	531656
489	533974	532067	533974
490	536432	534324	536432
491	537150	536707	537150
492	537928	537080	537928
493	538438	537932	538438
494	538737	538333	538737
495	539594	539127	539594
496	541215	539590	541215
497	542571	541282	542571
498	543014	542457	543014
499	543369	542962	543369
500	543809	546628	543815
501	546619	549525	546619
502	547293	546994	547293
503	549699	550523	549699
504	550490	551551	550490
505	551448	552623	551448
506	552652	555117	552652
507	555029	555493	555029
508	558006	555673	558006
509	559694	558162	559694
510	558208	558573	558208

ORF Nos	begin	end	potential start
511	561692	559899	561692
512	561412	561708	561412
513	563942	561777	563942
514	564969	563950	564969
515	566204	564936	566198
516	567717	566302	567717
517	568526	567708	568526
518	569467	568742	569467
519	571065	569431	571065
520	571828	571118	571783
521	572202	573308	572202
522	573146	575056	573146
523	575023	575916	575023
524	577891	576497	577891
525	578914	578204	578914
526	579924	578857	579924
527	580187	579858	580187
528	580017	580406	580017
529	581086	580187	581086
530	581367	581828	581367
531	581678	582367	581678
532	582361	583428	582361
533	584690	583431	584690
534	585237	584950	585237
535	585626	586888	585626
536	586846	587907	586888
537	589049	588180	589049
538	590500	589301	590455
539	590755	592458	590755
540	592526	592903	592526
541	592836	593747	592836
542	593747	594298	593747
543	594331	595947	594331
544	595905	596309	595905

ORF Nos	begin	end	potential start
545	596514	597215	596514
546	597184	597957	597184
547	597755	598612	597755
548	598602	599204	598602
549	599373	599939	599373
550	600903	602072	600903
551	602240	602587	602240
552	602637	603272	602637
553	603142	604512	603142
554	604627	605853	604627
555	605790	606620	605790
556	606571	607281	606571
557	609004	607355	609004
558	610906	609932	610906
559	611786	611004	611786
560	612333	611746	612333
561	613897	612341	613897
562	615179	616279	615179
563	616610	617383	616610
564	618796	617810	618796
565	620004	618826	620004
566	619649	619918	619649
567	621265	620021	621265
568	622359	621265	622359
569	623420	622560	623420
570	624297	623335	624297
571	624773	624174	624773
572	625029	625484	625029
573	625488	625883	625488
574	625892	626395	625892
575	626444	627790	626444
576	627912	628607	627930
577	628774	629697	628774
578	629660	631639	629660

ORF Nos	begin	end	potential start
579	631725	633551	631725
580	633520	636957	633520
581	637232	638098	637232
582	640648	639593	640648
583	640979	640728	640979
584	641327	641007	641327
585	641687	642283	641687
586	643023	642286	643023
587	643330	643076	643330
588	643704	643351	643704
589	645628	643676	645628
590	645783	645538	645756
591	646269	645793	646269
592	646751	646314	646751
593	647848	647045	647848
594	648393	650336	648393
595	651016	650420	651007
596	652956	651289	652956
597	653395	653126	653395
598	655740	654193	655740
599	656508	655966	656508
600	658140	657022	658140
601	660216	658525	660216
602	663238	660248	663238
603	664461	663157	664452
604	665735	664635	665735
605	666212	666994	666212
606	666998	667921	666998
607	667909	668568	667909
608	668502	669203	668502
609	669154	670893	669175
610	672226	670853	672226
611	671137	671424	671137
612	672453	673001	672453

ORF Nos	begin	end	potential start
613	673072	674721	673072
614	674549	674262	674549
615	675518	674796	675518
616	676083	675499	676083
617	676630	676067	676630
618	677016	676600	677016
619	677647	677015	677647
620	677990	678259	677990
621	679444	680097	679444
622	680097	680897	680097
623	681637	680849	681637
624	681409	682281	681409
625	682453	682821	682453
626	682763	683902	682763
627	684616	683969	684616
628	685169	684534	685169
629	685986	685117	685986
630	686278	687288	686278
631	687483	688151	687483
632	688740	689501	688740
633	690242	689622	690242
634	690470	691126	690470
635	692600	691497	692600
636	692674	695064	692674
637	695049	696032	695064
638	697964	696585	697964
639	699803	698274	699803
640	701926	699788	701926
641	703196	702567	703196
642	704221	703208	704221
643	704240	705289	704240
644	706070	705300	706070
645	706841	706254	706838
646	707596	706811	707596

ORF Nos	begin	end	potential start
647	708666	707677	708666
648	709793	709119	709793
649	711523	710132	711523
650	712236	711523	712236
651	714734	712125	714734
652	715759	714761	715759
653	717538	715886	717538
654	719113	720243	719113
655	720590	722422	720590
656	722406	723056	722406
657	723551	723120	723551
658	724246	723626	724246
659	724754	724251	724754
660	725868	724900	725868
661	727115	726270	727115
662	728126	727119	728126
663	728594	728208	728594
664	729614	728604	729614
665	729778	729533	729778
666	730149	729751	730149
667	730539	730174	730539
668	731983	730598	731983
669	732427	731996	732427
670	732917	732423	732917
671	733598	733320	733598
672	733869	733492	733869
673	734298	733900	734298
674	734858	734319	734858
675	735195	734863	735195
676	735578	735342	735578
677	735861	735604	735861
678	736492	736079	736492
679	737192	736524	737192
680	737555	737211	737555

ORF Nos	begin	end	potential start
681	738688	737837	738688
682	739048	738713	739048
683	739736	739065	739736
684	740477	739773	740477
685	740659	740958	740659
686	741722	740721	741722
687	742789	741827	742789
688	743618	742782	743618
689	744092	743634	744092
690	744604	744107	744604
691	744953	744498	744953
692	746608	744986	746608
693	747085	746621	747085
694	747974	747219	747974
695	748594	748169	748594
696	749145	748573	749145
697	749652	749957	749652
698	750446	749979	750446
699	751219	750446	751219
700	753042	751291	753042
701	754309	753020	754309
702	755120	756175	755120
703	756120	756485	756120
704	756499	760227	756499
705	761217	760297	761178
706	761297	761809	761330
707	761782	762282	761782
708	762260	762895	762299
709	762867	763316	762867
710	763780	763325	763780
711	763861	765168	763861
712	766809	765697	766809
713	768051	766888	768051
714	768566	768321	768566

ORF Nos	begin	end	potential start
715	769342	768551	769342
716	770532	769378	770532
717	771451	770804	771451
718	773058	771847	773058
719	773094	773456	773094
720	774376	773093	774376
721	775123	774380	775123
722	775398	774916	775398
723	775046	776077	775046
724	776070	777041	776070
725	777964	777536	777964
726	778176	777904	778176
727	778621	779334	778684
728	781173	780307	781173
729	781526	781116	781526
730	782784	781555	782784
731	783572	782805	783572
732	785032	783581	785032
733	786412	785360	786412
734	788429	786450	788429
735	788944	788528	788944
736	789758	788901	789758
737	790332	791504	790338
738	791846	792721	791846
739	792724	793569	792724
740	793580	794323	793580
741	794304	794843	794304
742	795217	795732	795217
743	795722	796795	795722
744	798735	797053	798735
745	799823	798681	799823
746	799297	799578	799297
747	801313	799808	801313
748	802453	801332	802453

ORF Nos	begin	end	potential start
749	803299	802457	803299
750	803811	803290	803811
751	805151	803826	805151
752	805860	805156	805860
753	806604	806332	806604
754	806913	806608	806913
755	808222	806903	808222
756	808751	808146	808751
757	809437	808673	809437
758	809939	809454	809939
759	811235	810213	811235
760	811779	813056	811779
761	812890	812516	812890
762	812954	813583	812954
763	813587	815023	813587
764	815420	815746	815420
765	816036	817010	816036
766	817111	817356	817111
767	817791	818609	817797
768	818609	819094	818609
769	819104	819823	819104
770	820722	819826	820722
771	822313	821000	822313
772	823503	822238	823503
773	823678	825612	823678
774	825461	826312	825461
775	827280	826645	827280
776	828604	827171	828604
777	830026	828713	830026
778	831047	830085	831047
779	831725	831051	831725
780	832220	833098	832220
781	833851	833396	833851
782	834068	835039	834068

ORF Nos	begin	end	potential start
783	835792	835127	835792
784	837624	836116	837624
785	838951	840882	838951
786	840869	842185	840869
787	841989	843455	841989
788	843242	844021	843242
789	845018	843987	844997
790	846174	844990	846174
791	848509	846311	848509
792	848568	849014	848568
793	849082	850488	849088
794	851512	850574	851512
795	852064	852447	852064
796	852398	853690	852398
797	855118	854243	855118
798	855751	855128	855751
799	856551	855829	856551
800	856730	858556	856730
801	858717	859601	858717
802	859591	860205	859591
803	861132	860284	861132
804	861426	861163	861426
805	861701	862921	861701
806	863026	864798	863026
807	864831	865256	864831
808	865226	866581	865226
809	866562	867119	866562
810	867025	867816	867025
811	867820	868497	867820
812	869743	868661	869743
813	870633	870094	870633
814	871929	870646	871929
815	872538	872086	872538
816	873908	872517	873908

ORF Nos	begin	end	potential start
817	874281	874670	874281
818	874582	875286	874582
819	877857	875377	877857
820	878446	879255	878446
821	880635	879268	880635
822	882524	880593	882524
823	882612	883319	882612
824	884155	883538	884155
825	884340	885611	884343
826	885722	887302	885722
827	887587	888153	887587
828	888627	888220	888627
829	889330	888716	889330
830	889898	889323	889898
831	891190	889898	891190
832	891828	891247	891828
833	892421	892017	892421
834	893116	892421	893116
835	892521	892925	892521
836	893392	895419	893392
837	895745	896527	895745
838	896668	897558	896668
839	897565	899442	897565
840	899420	900229	899420
841	903230	900237	903230
842	905081	903234	905081
843	906931	905045	906931
844	907248	907832	907299
845	907784	908128	907784
846	908132	908677	908132
847	908589	909320	908589
848	909405	911465	909405
849	911677	912360	911725
850	912303	912821	912303

ORF Nos	begin	end	potential start
851	912937	913983	912937
852	915128	914067	915128
853	916658	915303	916658
854	915627	915376	915627
855	917707	916853	917707
856	918837	917722	918837
857	919868	918837	919868
858	920434	919880	920434
859	921187	920438	921187
860	921959	921195	921959
861	923773	921995	923773
862	922146	922415	922146
863	923943	923674	923943
864	924077	925006	924077
865	925436	925083	925436
866	926524	925349	926524
867	927920	926433	927920
868	928319	927951	928319
869	928963	928334	928963
870	929248	930987	929248
871	930995	932059	930995
872	932121	933515	932175
873	932881	932513	932881
874	933485	935746	933485
875	935724	937082	935724
876	937229	938410	937229
877	938281	938805	938281
878	938809	939255	938824
879	939165	939782	939165
880	939760	940791	939790
881	940822	941106	940822
882	940977	941351	940977
883	942537	941623	942429
884	942784	942500	942763

ORF Nos	begin	end	potential start
885	943149	942799	943149
886	943799	943029	943799
887	944055	943732	944055
888	944413	943994	944404
889	945395	944556	945395
890	945853	945389	945853
891	946392	945751	946392
892	947410	948081	947431
893	949871	948915	949871
894	951058	949868	951058
895	951249	950959	951249
896	951664	952134	951664
897	952674	952165	952674
898	953491	952589	953491
899	955324	953495	955324
900	955823	955281	955823
901	957082	955847	957082
902	957902	957270	957902
903	959231	957906	959231
904	959376	960284	959376
905	960266	961669	960347
906	961856	964765	961856
907	966855	965395	966855
908	968204	966975	968204
909	968791	968237	968791
910	969498	968731	969498
911	969858	969511	969858
912	970118	969762	970118
913	970593	970300	970593
914	971261	970542	971261
915	971680	971123	971680
916	971876	975100	971876
917	975419	976516	975419
918	976584	978320	976584

ORF Nos	begin	end	potential start
919	977680	977231	977680
920	978399	980738	978399
921	980756	981928	980756
922	982974	981931	982962
923	984120	983119	984120
924	985502	984120	985502
925	987180	985882	987180
926	987172	987444	987172
927	989846	989049	989846
928	991048	989846	991048
929	991638	990955	991638
930	991794	992498	991794
931	993619	993041	993619
932	993530	994792	993548
933	995970	994795	995970
934	996857	995739	996857
935	997603	996782	997603
936	998969	997572	998969
937	998896	1000023	998896
938	1000087	1001340	1000087
939	1001357	1001818	1001357
940	1003288	1001873	1003288
941	1003487	1004146	1003496
942	1004485	1005639	1004689
943	1005643	1005972	1005643
944	1006784	1006116	1006784
945	1007563	1006769	1007563
946	1009226	1007568	1009226
947	1009989	1009336	1009989
948	1015852	1016337	1015852
949	1016561	1016181	1016561
950	1016297	1017532	1016297
951	1016802	1016452	1016802
952	1018993	1017701	1018993

ORF Nos	begin	end	potential start
953	1019454	1019137	1019454
954	1020764	1019562	1020764
955	1021405	1021037	1021405
956	1021821	1024286	1021821
957	1024697	1024248	1024697
958	1025569	1024508	1025551
959	1026969	1025590	1026969
960	1027789	1026947	1027789
961	1031199	1027945	1031199
962	1031717	1031172	1031717
963	1033057	1031612	1033057
964	1033425	1033039	1033425
965	1033784	1033200	1033784
966	1033963	1036038	1033963
967	1036945	1036010	1036945
968	1037110	1037679	1037110
969	1037696	1037944	1037696
970	1038916	1037975	1038916
971	1040582	1039026	1040582
972	1040997	1042337	1040997
973	1042357	1043403	1042357
974	1043367	1044623	1043367
975	1044607	1045362	1044607
976	1045384	1046538	1045384
977	1046447	1047517	1046447
978	1047521	1049956	1047521
979	1050611	1050036	1050611
980	1050925	1050566	1050925
981	1051728	1051090	1051728
982	1051743	1052063	1051743
983	1052101	1053126	1052101
984	1054201	1053107	1054201
985	1054242	1055555	1054242
986	1055483	1055908	1055483

ORF Nos	begin	end	potential start
987	1056609	1056965	1056609
988	1056961	1058232	1056985
989	1058238	1058687	1058238
990	1059371	1058727	1059371
991	1059526	1060578	1059526
992	1061553	1060579	1061553
993	1061674	1062411	1061674
994	1062377	1064077	1062377
995	1064116	1065243	1064116
996	1067451	1065178	1067451
997	1068065	1067376	1068065
998	1068209	1068706	1068230
999	1069958	1068819	1069958
1000	1071163	1070033	1071163
1001	1072438	1071332	1072438
1002	1072997	1073476	1072997
1003	1074239	1075864	1074239
1004	1076790	1075867	1076790
1005	1077268	1076573	1077268
1006	1077999	1078724	1077999
1007	1079088	1078672	1079088
1008	1079642	1079944	1079642
1009	1080501	1079995	1080468
1010	1080775	1081341	1080775
1011	1083158	1081350	1083158
1012	1084677	1083235	1084677
1013	1085648	1084632	1085648
1014	1086117	1086737	1086117
1015	1086692	1087897	1086692
1016	1088646	1089005	1088646
1017	1089146	1089805	1089146
1018	1092931	1089890	1092931
1019	1093179	1092889	1093179
1020	1093584	1094204	1093584

ORF Nos	begin	end	potential start
1021	1095619	1094192	1095619
1022	1096074	1096628	1096074
1023	1096633	1097082	1096633
1024	1097266	1097601	1097266
1025	1097622	1097867	1097622
1026	1097886	1098392	1097886
1027	1099521	1099279	1099521
1028	1099689	1101053	1099704
1029	1102192	1101107	1102192
1030	1104950	1102116	1104950
1031	1106508	1104946	1106508
1032	1106722	1107249	1106722
1033	1107463	1108101	1107463
1034	1108041	1108421	1108041
1035	1108520	1113370	1108520
1036	1114958	1113447	1114958
1037	1116915	1115071	1116915
1038	1118183	1116894	1118183
1039	1118846	1120030	1118846
1040	1120040	1120522	1120040
1041	1120510	1121430	1120510
1042	1121321	1121866	1121321
1043	1122123	1122899	1122123
1044	1124842	1125564	1124842
1045	1126526	1125579	1126526
1046	1126519	1127676	1126519
1047	1127672	1128571	1127672
1048	1130230	1131336	1130230
1049	1131480	1132553	1131480
1050	1132830	1133843	1132830
1051	1134121	1134855	1134121
1052	1134642	1135592	1134642
1053	1135964	1135653	1135964
1054	1137132	1135954	1137132

ORF Nos	begin	end	potential start
1055	1137169	1140102	1137169
1056	1141365	1140112	1141344
1057	1142150	1141356	1142150
1058	1142520	1145660	1142520
1059	1145627	1146721	1145627
1060	1146862	1147545	1146862
1061	1147666	1148190	1147666
1062	1148514	1148224	1148514
1063	1149136	1148348	1149136
1064	1149702	1149166	1149702
1065	1150031	1150591	1150031
1066	1150785	1151147	1150785
1067	1151165	1152181	1151165
1068	1152522	1154591	1152522
1069	1155666	1154566	1155666
1070	1156743	1155670	1156740
1071	1156859	1157815	1156859
1072	1157982	1160735	1157982
1073	1162620	1160917	1162620
1074	1162970	1162590	1162970
1075	1163532	1164020	1163532
1076	1163995	1164294	1163995
1077	1165569	1165030	1165569
1078	1166108	1165566	1166108
1079	1166644	1166141	1166644
1080	1167055	1168374	1167055
1081	1169218	1168337	1169218
1082	1169823	1169218	1169823
1083	1171324	1170572	1171324
1084	1172085	1171177	1172085
1085	1172394	1173773	1172394
1086	1175209	1173881	1175209
1087	1175555	1175127	1175360
1088	1175778	1177043	1175778

ORF Nos	begin	end	potential start
1089	1177177	1179048	1177177
1090	1179156	1180085	1179156
1091	1180045	1180779	1180045
1092	1181942	1180788	1181942
1093	1182296	1181961	1182296
1094	1183844	1182300	1183844
1095	1184420	1183848	1184420
1096	1185382	1184366	1185382
1097	1185858	1185226	1185858
1098	1186164	1186481	1186185
1099	1187386	1186484	1187386
1100	1187370	1189028	1187370
1101	1189321	1190889	1189321
1102	1191142	1192146	1191142
1103	1191974	1191729	1191974
1104	1193815	1192991	1193815
1105	1195702	1194248	1195702
1106	1196303	1195716	1196303
1107	1196831	1196337	1196831
1108	1197807	1196746	1197651
1109	1198740	1197883	1198668
1110	1200232	1198721	1200232
1111	1201286	1200135	1201286
1112	1202386	1201259	1202350
1113	1202901	1202350	1202901
1114	1204162	1202816	1204162
1115	1203177	1203464	1203177
1116	1205028	1204180	1205028
1117	1206392	1204878	1206392
1118	1206742	1206086	1206742
1119	1207872	1206724	1207872
1120	1208852	1207851	1208852
1121	1210518	1209742	1210518
1122	1210703	1211494	1210703

ORF Nos	begin	end	potential start
1123	1211870	1212754	1211870
1124	1212742	1214064	1212742
1125	1214046	1214858	1214046
1126	1215551	1216318	1215551
1127	1216493	1216849	1216493
1128	1217183	1219612	1217183
1129	1220068	1219673	1220068
1130	1219710	1220669	1219710
1131	1220630	1221376	1220630
1132	1221645	1223681	1221645
1133	1223894	1224988	1223900
1134	1225000	1225830	1225000
1135	1227810	1225879	1227810
1136	1226528	1226908	1226528
1137	1229972	1228311	1229972
1138	47569	47018	47569
1139	49980	49117	49980
1140	53356	52898	53356
1141	54477	54884	54477
1142	63753	63998	63753
1143	77164	77487	77164
1144	79724	79302	79724
1145	88721	88951	88721
1146	94067	94429	94067
1147	122832	123341	122832
1148	147536	147234	147536
1149	158990	159346	158990
1150	168470	168979	168470
1151	169183	169452	169204
1152	171785	171504	171785
1153	172518	171775	172518
1154	193599	194045	193599
1155	195704	196075	195704
1156	210687	210145	210684

ORF Nos	begin	end	potential start
1157	211100	210708	211100
1158	215420	215088	215420
1159	217914	218246	217914
1160	218925	218701	218925
1161	223785	223525	223785
1162	224271	223999	224271
1163	228691	228407	228691
1164	235050	235334	235050
1165	252308	253021	252308
1166	258280	258912	258280
1167	261325	261567	261325
1168	268195	268878	268195
1169	269447	268881	269447
1170	271263	271538	271263
1171	271957	272346	271957
1172	274176	274550	274176
1173	275736	275314	275736
1174	276490	276927	276490
1175	277577	277861	277577
1176	288163	287909	288163
1177	290130	289789	290130
1178	290989	291225	290989
1179	291372	291860	291372
1180	311239	311622	311239
1181	328665	328384	328665
1182	337348	338289	337348
1183	364764	364369	364764
1184	389623	390135	389623
1185	393729	394343	393729
1186	407379	407621	407379
1187	410944	410708	410944
1188	427632	427988	427632
1189	428172	428486	428172
1190	436761	437246	436761

ORF Nos	begin	end	potential start
1191	460911	461159	460911
1192	477597	477313	477597
1193	487303	487001	487303
1194	487764	487534	487764
1195	498502	499017	498502
1196	499795	500466	499795
1197	571928	572344	571928
1198	572367	572131	572367
1199	588184	587915	588184
1200	600587	600907	600587
1201	609731	608895	609731
1202	614039	614755	614039
1203	614823	615152	614823
1204	638244	638831	638244
1205	638819	639094	638819
1206	639073	639636	639073
1207	647901	648236	647901
1208	678510	679469	678510
1209	688178	688732	688178
1210	696045	696563	696045
1211	708998	708588	708998
1212	709808	710089	709808
1213	718240	717737	718240
1214	737828	737565	737828
1215	779502	780257	779502
1216	806310	805864	806310
1217	820931	820707	820931
1218	837696	839096	837696
1219	883307	883549	883307
1220	892010	891726	892010
1221	893277	893564	893277
1222	936998	937225	936998
1223	946865	947419	946865
1224	975187	975411	975187

ORF Nos	begin	end	potential start
1225	985882	985517	985882
1226	987713	987180	987713
1227	988215	987733	988215
1228	988754	988530	988754
1229	992542	992841	992542
1230	992759	993067	992759
1231	1004247	1004528	1004268
1232	1015013	1014294	1015013
1233	1056147	1056545	1056147
1234	1077682	1078035	1077682
1235	1088121	1088381	1088121
1236	1098430	1098852	1098430
1237	1098798	1099319	1098798
1238	1123198	1123515	1123198
1239	1123606	1124256	1123606
1240	1124453	1124797	1124453
1241	1129253	1129567	1129253
1242	1164947	1164474	1164947
1243	1170457	1170053	1170457
1244	1172342	1171863	1172342
1245	1192155	1192835	1192155
1246	1192759	1192992	1192759
1247	1193861	1194142	1193861
1248	1194036	1193779	1194036
1249	1209748	1209053	1209748
1250	1215111	1215419	1215111
1251	1216302	1216538	1216302
1252	1228072	1227818	1228072
1253	1228304	1228080	1228304
1254	26599	26222	26599
1255	27609	27367	27609
1256	67206	66967	67197
1257	70612	70352	70588
1258	132703	132945	132703

ORF Nos	begin	end	potential start
1259	178073	178393	178073
1260	208576	208349	208576
1261	209156	208929	209156
1262	209263	209024	209263
1263	210304	210639	210304
1264	299009	299452	299030
1265	352106	351717	352061
1266	420182	419949	420170
1267	553602	553381	553602
1268	556538	556807	556538
1269	594348	593797	594342
1270	595169	594876	595160
1271	662148	662381	662160
1272	706528	706893	706528
1273	803315	803650	803339
1274	849551	849306	849551
1275	913676	913275	913676
1276	927087	926836	927087
1277	930587	930360	930587
1278	986531	986764	986531
1279	996229	996486	996229
1280	1000373	1000002	1000334
1281	1010291	1010037	1010273
1282	1011128	1010793	1011128
1283	1012924	1012694	1012924
1284	1028659	1028913	1028659
1285	1086481	1086762	1086481
1286	1118658	1118879	1118658
1287	1170098	1169835	1170098
1288	1180828	1181184	1180828
1289	1182658	1183035	1182658
1290	1195076	1194795	1195055
1291	1195890	1196183	1195890
1292	189042	188809	189030

ORF Nos	begin	end	potential start
1293	691250	691567	691250
1294	914544	914780	914556
1295	928525	928833	928579
1296	1040685	1040948	1040712
1297	377646	378068	377646

Table 4

<i>SEQ ID NO (ORF)</i>	<i>Fp</i>	<i>Fd</i>	<i>Bp</i>	<i>Bd</i>
2	1292	1293	3796	3797
3	1294	1295	3798	3799
4	1296	1297	3800	3801
5	1298	1299	3802	3803
6	1300	1301	3804	3805
7	1302	1303	3806	3807
8	1304	1305	3808	3809
9	1306	1307	3810	3811
10	1308	1309	3812	3813
11	1310	1311	3814	3815
12	1312	1313	3816	3817
13	1314	1315	3818	3819
14	1316	1317	3820	3821
15	1318	1319	3822	3823
16	1320	1321	3824	3825
17	1322	1323	3826	3827
18	1324	1325	3828	3829
19	1326	1327	3830	3831
20	1328	1329	3832	3833
21	1330	1331	3834	3835
22	1332	1333	3836	3837
23	1334	1335	3838	3839
24	1336	1337	3840	3841
25	1338	1339	3842	3843
26	1340	1341	3844	3845
27	1342	1343	3846	3847
28	1344	1345	3848	3849
29	1346	1347	3850	3851
30	1348	1349	3852	3853
31	1350	1351	3854	3855
32	1352	1353	3856	3857
33	1354	1355	3858	3859
34	1358	1359	3862	3863

35	1356	1357	3860	3861
36	1360	1361	3864	3865
37	1362	1363	3866	3867
38	1364	1365	3868	3869
39	1366	1367	3870	3871
40	1368	1369	3872	3873
41	1370	1371	3874	3875
42	1374	1375	3878	3879
43	1376	1377	3880	3881
44	1380	1381	3884	3885
45	1382	1383	3886	3887
46	1386	1387	3890	3891
47	1388	1389	3892	3893
48	1392	1393	3896	3897
49	1394	1395	3898	3899
50	1396	1397	3900	3901
51	1398	1399	3902	3903
52	1402	1403	3906	3907
53	1400	1401	3904	3905
54	1404	1405	3908	3909
55	1406	1407	3910	3911
56	1410	1411	3914	3915
57	1412	1413	3916	3917
58	1414	1415	3918	3919
59	1416	1417	3920	3921
60	1418	1419	3922	3923
61	1420	1421	3924	3925
62	1422	1423	3926	3927
63	1424	1425	3928	3929
64	1426	1427	3930	3931
65	1428	1429	3932	3933
66	1430	1431	3934	3935
67	1432	1433	3936	3937
68	1434	1435	3938	3939
69	1438	1439	3942	3943

70	1440	1441	3944	3945
71	1444	1445	3948	3949
72	1446	1447	3950	3951
73	1448	1449	3952	3953
74	1450	1451	3954	3955
75	1452	1453	3956	3957
76	1454	1455	3958	3959
77	1456	1457	3960	3961
78	1458	1459	3962	3963
79	1460	1461	3964	3965
80	1462	1463	3966	3967
81	1464	1465	3968	3969
82	1468	1469	3972	3973
83	1470	1471	3974	3975
84	1472	1473	3976	3977
85	1476	1477	3980	3981
86	1478	1479	3982	3983
87	1480	1481	3984	3985
88	1482	1483	3986	3987
89	1484	1485	3988	3989
90	1486	1487	3990	3991
91	1488	1489	3992	3993
92	1490	1491	3994	3995
93	1492	1493	3996	3997
94	1494	1495	3998	3999
95	1496	1497	4000	4001
96	1498	1499	4002	4003
97	1500	1501	4004	4005
98	1502	1503	4006	4007
99	1504	1505	4008	4009
100	1506	1507	4010	4011
101	1508	1509	4012	4013
102	1510	1511	4014	4015
103	1512	1513	4016	4017
104	1514	1515	4018	4019

105	1516	1517	4020	4021
106	1518	1519	4022	4023
107	1520	1521	4024	4025
108	1522	1523	4026	4027
109	1524	1525	4028	4029
110	1526	1527	4030	4031
111	1530	1531	4034	4035
112	1532	1533	4036	4037
113	1534	1535	4038	4039
114	1536	1537	4040	4041
115	1538	1539	4042	4043
116	1540	1541	4044	4045
117	1542	1543	4046	4047
118	1544	1545	4048	4049
119	1546	1547	4050	4051
120	1548	1549	4052	4053
121	1550	1551	4054	4055
122	1552	1553	4056	4057
123	1554	1555	4058	4059
124	1556	1557	4060	4061
125	1558	1559	4062	4063
126	1562	1563	4066	4067
127	1564	1565	4068	4069
128	1566	1567	4070	4071
129	1568	1569	4072	4073
130	1570	1571	4074	4075
131	1572	1573	4076	4077
132	1574	1575	4078	4079
133	1576	1577	4080	4081
134	1580	1581	4084	4085
135	1582	1583	4086	4087
136	1584	1585	4088	4089
137	1586	1587	4090	4091
138	1588	1589	4092	4093
139	1590	1591	4094	4095

140	1592	1593	4096	4097
141	1594	1595	4098	4099
142	1596	1597	4100	4101
143	1598	1599	4102	4103
144	1604	1605	4108	4109
145	1606	1607	4110	4111
146	1612	1613	4116	4117
147	1614	1615	4118	4119
148	1616	1617	4120	4121
149	1618	1619	4122	4123
150	1620	1621	4124	4125
151	1624	1625	4128	4129
152	1622	1623	4126	4127
153	1626	1627	4130	4131
154	1628	1629	4132	4133
155	1630	1631	4134	4135
156	1632	1633	4136	4137
157	1634	1635	4138	4139
158	1636	1637	4140	4141
159	1638	1639	4142	4143
160	1640	1641	4144	4145
161	1642	1643	4146	4147
162	1644	1645	4148	4149
163	1646	1647	4150	4151
164	1648	1649	4152	4153
165	1650	1651	4154	4155
166	1652	1653	4156	4157
167	1656	1657	4160	4161
168	1658	1659	4162	4163
169	1662	1663	4166	4167
170	1664	1665	4168	4169
171	1666	1667	4170	4171
172	1668	1669	4172	4173
173	1670	1671	4174	4175
174	1672	1673	4176	4177

175	1674	1675	4178	4179
176	1676	1677	4180	4181
177	1678	1679	4182	4183
178	1684	1685	4188	4189
179	1686	1687	4190	4191
180	1688	1689	4192	4193
181	1690	1691	4194	4195
182	1694	1695	4198	4199
183	1696	1697	4200	4201
184	1698	1699	4202	4203
185	1700	1701	4204	4205
186	1704	1705	4208	4209
187	1708	1709	4212	4213
188	1710	1711	4214	4215
189	1712	1713	4216	4217
190	1714	1715	4218	4219
191	1720	1721	4224	4225
192	1722	1723	4226	4227
193	1724	1725	4228	4229
194	1726	1727	4230	4231
195	1728	1729	4232	4233
196	1732	1733	4236	4237
197	1734	1735	4238	4239
198	1736	1737	4240	4241
199	1738	1739	4242	4243
200	1740	1741	4244	4245
201	1742	1743	4246	4247
202	1744	1745	4248	4249
203	1746	1747	4250	4251
204	1750	1751	4254	4255
205	1752	1753	4256	4257
206	1754	1755	4258	4259
207	1756	1757	4260	4261
208	1758	1759	4262	4263
209	1760	1761	4264	4265

210	1762	1763	4266	4267
211	1764	1765	4268	4269
212	1766	1767	4270	4271
213	1768	1769	4272	4273
214	1770	1771	4274	4275
215	1772	1773	4276	4277
216	1774	1775	4278	4279
217	1776	1777	4280	4281
218	1778	1779	4282	4283
219	1782	1783	4286	4287
220	1784	1785	4288	4289
221	1786	1787	4290	4291
222	1788	1789	4292	4293
223	1790	1791	4294	4295
224	1792	1793	4296	4297
225	1796	1797	4300	4301
226	1800	1801	4304	4305
227	1802	1803	4306	4307
228	1804	1805	4308	4309
229	1806	1807	4310	4311
230	1808	1809	4312	4313
231	1810	1811	4314	4315
232	1812	1813	4316	4317
233	1818	1819	4322	4323
234	1824	1825	4328	4329
235	1826	1827	4330	4331
236	1828	1829	4332	4333
237	1834	1835	4338	4339
238	1836	1837	4340	4341
239	1840	1841	4344	4345
240	1842	1843	4346	4347
241	1846	1847	4350	4351
242	1848	1849	4352	4353
243	1850	1851	4354	4355
244	1852	1853	4356	4357

245	1854	1855	4358	4359
246	1856	1857	4360	4361
247	1858	1859	4362	4363
248	1860	1861	4364	4365
249	1862	1863	4366	4367
250	1864	1865	4368	4369
251	1866	1867	4370	4371
252	1868	1869	4372	4373
253	1872	1873	4376	4377
254	1876	1877	4380	4381
255	1874	1875	4378	4379
256	1878	1879	4382	4383
257	1886	1887	4390	4391
258	1888	1889	4392	4393
259	1890	1891	4394	4395
260	1892	1893	4396	4397
261	1896	1897	4400	4401
262	1894	1895	4398	4399
263	1898	1899	4402	4403
264	1900	1901	4404	4405
265	1902	1903	4406	4407
266	1904	1905	4408	4409
267	1906	1907	4410	4411
268	1908	1909	4412	4413
269	1910	1911	4414	4415
270	1912	1913	4416	4417
271	1914	1915	4418	4419
272	1916	1917	4420	4421
273	1918	1919	4422	4423
274	1920	1921	4424	4425
275	1922	1923	4426	4427
276	1924	1925	4428	4429
277	1926	1927	4430	4431
278	1928	1929	4432	4433
279	1930	1931	4434	4435

280	1934	1935	4438	4439
281	1936	1937	4440	4441
282	1938	1939	4442	4443
283	1940	1941	4444	4445
284	1942	1943	4446	4447
285	1944	1945	4448	4449
286	1946	1947	4450	4451
287	1948	1949	4452	4453
288	1950	1951	4454	4455
289	1952	1953	4456	4457
290	1954	1955	4458	4459
291	1956	1957	4460	4461
292	1958	1959	4462	4463
293	1960	1961	4464	4465
294	1962	1963	4466	4467
295	1964	1965	4468	4469
296	1966	1967	4470	4471
297	1970	1971	4474	4475
298	1972	1973	4476	4477
299	1974	1975	4478	4479
300	1976	1977	4480	4481
301	1978	1979	4482	4483
302	1980	1981	4484	4485
303	1984	1985	4488	4489
304	1986	1987	4490	4491
305	1988	1989	4492	4493
306	1990	1991	4494	4495
307	1992	1993	4496	4497
308	1994	1995	4498	4499
309	1996	1997	4500	4501
310	1998	1999	4502	4503
311	2000	2001	4504	4505
312	2002	2003	4506	4507
313	2004	2005	4508	4509
314	2006	2007	4510	4511

315	2008	2009	4512	4513
316	2010	2011	4514	4515
317	2012	2013	4516	4517
318	2014	2015	4518	4519
319	2016	2017	4520	4521
320	2018	2019	4522	4523
321	2020	2021	4524	4525
322	2022	2023	4526	4527
323	2026	2027	4530	4531
324	2024	2025	4528	4529
325	2028	2029	4532	4533
326	2030	2031	4534	4535
327	2032	2033	4536	4537
328	2034	2035	4538	4539
329	2038	2039	4542	4543
330	2040	2041	4544	4545
331	2042	2043	4546	4547
332	2044	2045	4548	4549
333	2046	2047	4550	4551
334	2048	2049	4552	4553
335	2050	2051	4554	4555
336	2052	2053	4556	4557
337	2054	2055	4558	4559
338	2056	2057	4560	4561
339	2058	2059	4562	4563
340	2060	2061	4564	4565
341	2062	2063	4566	4567
342	2064	2065	4568	4569
343	2066	2067	4570	4571
344	2068	2069	4572	4573
345	2070	2071	4574	4575
346	2072	2073	4576	4577
347	2074	2075	4578	4579
348	2076	2077	4580	4581
349	2078	2079	4582	4583

350	2080	2081	4584	4585
351	2082	2083	4586	4587
352	2084	2085	4588	4589
353	2088	2089	4592	4593
354	2090	2091	4594	4595
355	2092	2093	4596	4597
356	2094	2095	4598	4599
357	2096	2097	4600	4601
358	2100	2101	4604	4605
359	2102	2103	4606	4607
360	2104	2105	4608	4609
361	2106	2107	4610	4611
362	2108	2109	4612	4613
363	2110	2111	4614	4615
364	2112	2113	4616	4617
365	2114	2115	4618	4619
366	2116	2117	4620	4621
367	2118	2119	4622	4623
368	2120	2121	4624	4625
369	2122	2123	4626	4627
370	2124	2125	4628	4629
371	2128	2129	4632	4633
372	2130	2131	4634	4635
373	2134	2135	4638	4639
374	2136	2137	4640	4641
375	2138	2139	4642	4643
376	2140	2141	4644	4645
377	2142	2143	4646	4647
378	2144	2145	4648	4649
379	2146	2147	4650	4651
380	2148	2149	4652	4653
381	2150	2151	4654	4655
382	2152	2153	4656	4657
383	2154	2155	4658	4659
384	2156	2157	4660	4661

385	2158	2159	4662	4663
386	2160	2161	4664	4665
387	2162	2163	4666	4667
388	2164	2165	4668	4669
389	2170	2171	4674	4675
390	2172	2173	4676	4677
391	2174	2175	4678	4679
392	2176	2177	4680	4681
393	2178	2179	4682	4683
394	2180	2181	4684	4685
395	2182	2183	4686	4687
396	2186	2187	4690	4691
397	2190	2191	4694	4695
398	2188	2189	4692	4693
399	2194	2195	4698	4699
400	2192	2193	4696	4697
401	2196	2197	4700	4701
402	2200	2201	4704	4705
403	2198	2199	4702	4703
404	2202	2203	4706	4707
405	2204	2205	4708	4709
406	2206	2207	4710	4711
407	2208	2209	4712	4713
408	2210	2211	4714	4715
409	2212	2213	4716	4717
410	2214	2215	4718	4719
411	2216	2217	4720	4721
412	2218	2219	4722	4723
413	2220	2221	4724	4725
414	2222	2223	4726	4727
415	2224	2225	4728	4729
416	2226	2227	4730	4731
417	2228	2229	4732	4733
418	2230	2231	4734	4735
419	2232	2233	4736	4737

420	2234	2235	4738	4739
421	2236	2237	4740	4741
422	2238	2239	4742	4743
423	2242	2243	4746	4747
424	2244	2245	4748	4749
425	2246	2247	4750	4751
426	2248	2249	4752	4753
427	2250	2251	4754	4755
428	2252	2253	4756	4757
429	2254	2255	4758	4759
430	2256	2257	4760	4761
431	2258	2259	4762	4763
432	2260	2261	4764	4765
433	2262	2263	4766	4767
434	2266	2267	4770	4771
435	2264	2265	4768	4769
436	2268	2269	4772	4773
437	2270	2271	4774	4775
438	2272	2273	4776	4777
439	2274	2275	4778	4779
440	2278	2279	4782	4783
441	2280	2281	4784	4785
442	2282	2283	4786	4787
443	2284	2285	4788	4789
444	2286	2287	4790	4791
445	2288	2289	4792	4793
446	2290	2291	4794	4795
447	2292	2293	4796	4797
448	2294	2295	4798	4799
449	2296	2297	4800	4801
450	2298	2299	4802	4803
451	2304	2305	4808	4809
452	2306	2307	4810	4811
453	2308	2309	4812	4813
454	2310	2311	4814	4815

455	2312	2313	4816	4817
456	2314	2315	4818	4819
457	2316	2317	4820	4821
458	2318	2319	4822	4823
459	2320	2321	4824	4825
460	2322	2323	4826	4827
461	2324	2325	4828	4829
462	2326	2327	4830	4831
463	2328	2329	4832	4833
464	2332	2333	4836	4837
465	2334	2335	4838	4839
466	2338	2339	4842	4843
467	2340	2341	4844	4845
468	2342	2343	4846	4847
469	2344	2345	4848	4849
470	2346	2347	4850	4851
471	2348	2349	4852	4853
472	2350	2351	4854	4855
473	2352	2353	4856	4857
474	2356	2357	4860	4861
475	2354	2355	4858	4859
476	2358	2359	4862	4863
477	2360	2361	4864	4865
478	2362	2363	4866	4867
479	2364	2365	4868	4869
480	2366	2367	4870	4871
481	2368	2369	4872	4873
482	2370	2371	4874	4875
483	2372	2373	4876	4877
484	2374	2375	4878	4879
485	2376	2377	4880	4881
486	2378	2379	4882	4883
487	2380	2381	4884	4885
488	2382	2383	4886	4887
489	2384	2385	4888	4889

490	2386	2387	4890	4891
491	2388	2389	4892	4893
492	2390	2391	4894	4895
493	2392	2393	4896	4897
494	2394	2395	4898	4899
495	2396	2397	4900	4901
496	2398	2399	4902	4903
497	2400	2401	4904	4905
498	2402	2403	4906	4907
499	2404	2405	4908	4909
500	2406	2407	4910	4911
501	2408	2409	4912	4913
502	2410	2411	4914	4915
503	2412	2413	4916	4917
504	2414	2415	4918	4919
505	2416	2417	4920	4921
506	2418	2419	4922	4923
507	2420	2421	4924	4925
508	2422	2423	4926	4927
509	2426	2427	4930	4931
510	2424	2425	4928	4929
511	2430	2431	4934	4935
512	2428	2429	4932	4933
513	2432	2433	4936	4937
514	2434	2435	4938	4939
515	2436	2437	4940	4941
516	2438	2439	4942	4943
517	2440	2441	4944	4945
518	2442	2443	4946	4947
519	2444	2445	4948	4949
520	2446	2447	4950	4951
521	2450	2451	4954	4955
522	2454	2455	4958	4959
523	2456	2457	4960	4961
524	2458	2459	4962	4963

525	2460	2461	4964	4965
526	2462	2463	4966	4967
527	2466	2467	4970	4971
528	2464	2465	4968	4969
529	2468	2469	4972	4973
530	2470	2471	4974	4975
531	2472	2473	4976	4977
532	2474	2475	4978	4979
533	2476	2477	4980	4981
534	2478	2479	4982	4983
535	2480	2481	4984	4985
536	2482	2483	4986	4987
537	2486	2487	4990	4991
538	2488	2489	4992	4993
539	2490	2491	4994	4995
540	2492	2493	4996	4997
541	2494	2495	4998	4999
542	2496	2497	5000	5001
543	2498	2499	5002	5003
544	2500	2501	5004	5005
545	2502	2503	5006	5007
546	2504	2505	5008	5009
547	2506	2507	5010	5011
548	2508	2509	5012	5013
549	2510	2511	5014	5015
550	2514	2515	5018	5019
551	2516	2517	5020	5021
552	2518	2519	5022	5023
553	2520	2521	5024	5025
554	2522	2523	5026	5027
555	2524	2525	5028	5029
556	2526	2527	5030	5031
557	2528	2529	5032	5033
558	2532	2533	5036	5037
559	2534	2535	5038	5039

560	2536	2537	5040	5041
561	2538	2539	5042	5043
562	2544	2545	5048	5049
563	2546	2547	5050	5051
564	2548	2549	5052	5053
565	2552	2553	5056	5057
566	2550	2551	5054	5055
567	2554	2555	5058	5059
568	2556	2557	5060	5061
569	2558	2559	5062	5063
570	2560	2561	5064	5065
571	2562	2563	5066	5067
572	2564	2565	5068	5069
573	2566	2567	5070	5071
574	2568	2569	5072	5073
575	2570	2571	5074	5075
576	2572	2573	5076	5077
577	2574	2575	5078	5079
578	2576	2577	5080	5081
579	2578	2579	5082	5083
580	2580	2581	5084	5085
581	2582	2583	5086	5087
582	2590	2591	5094	5095
583	2592	2593	5096	5097
584	2594	2595	5098	5099
585	2596	2597	5100	5101
586	2598	2599	5102	5103
587	2600	2601	5104	5105
588	2602	2603	5106	5107
589	2604	2605	5108	5109
590	2606	2607	5110	5111
591	2608	2609	5112	5113
592	2610	2611	5114	5115
593	2612	2613	5116	5117
594	2616	2617	5120	5121

595	2618	2619	5122	5123
596	2620	2621	5124	5125
597	2622	2623	5126	5127
598	2624	2625	5128	5129
599	2626	2627	5130	5131
600	2628	2629	5132	5133
601	2630	2631	5134	5135
602	2632	2633	5136	5137
603	2634	2635	5138	5139
604	2636	2637	5140	5141
605	2638	2639	5142	5143
606	2640	2641	5144	5145
607	2642	2643	5146	5147
608	2644	2645	5148	5149
609	2646	2647	5150	5151
610	2650	2651	5154	5155
611	2648	2649	5152	5153
612	2652	2653	5156	5157
613	2654	2655	5158	5159
614	2656	2657	5160	5161
615	2658	2659	5162	5163
616	2660	2661	5164	5165
617	2662	2663	5166	5167
618	2664	2665	5168	5169
619	2666	2667	5170	5171
620	2668	2669	5172	5173
621	2672	2673	5176	5177
622	2674	2675	5178	5179
623	2678	2679	5182	5183
624	2676	2677	5180	5181
625	2680	2681	5184	5185
626	2682	2683	5186	5187
627	2684	2685	5188	5189
628	2686	2687	5190	5191
629	2688	2689	5192	5193

630	2690	2691	5194	5195
631	2692	2693	5196	5197
632	2696	2697	5200	5201
633	2698	2699	5202	5203
634	2700	2701	5204	5205
635	2702	2703	5206	5207
636	2704	2705	5208	5209
637	2706	2707	5210	5211
638	2710	2711	5214	5215
639	2712	2713	5216	5217
640	2714	2715	5218	5219
641	2716	2717	5220	5221
642	2718	2719	5222	5223
643	2720	2721	5224	5225
644	2722	2723	5226	5227
645	2724	2725	5228	5229
646	2726	2727	5230	5231
647	2728	2729	5232	5233
648	2732	2733	5236	5237
649	2736	2737	5240	5241
650	2738	2739	5242	5243
651	2740	2741	5244	5245
652	2742	2743	5246	5247
653	2744	2745	5248	5249
654	2748	2749	5252	5253
655	2750	2751	5254	5255
656	2752	2753	5256	5257
657	2754	2755	5258	5259
658	2756	2757	5260	5261
659	2758	2759	5262	5263
660	2760	2761	5264	5265
661	2762	2763	5266	5267
662	2764	2765	5268	5269
663	2766	2767	5270	5271
664	2768	2769	5272	5273

665	2770	2771	5274	5275
666	2772	2773	5276	5277
667	2774	2775	5278	5279
668	2776	2777	5280	5281
669	2778	2779	5282	5283
670	2780	2781	5284	5285
671	2782	2783	5286	5287
672	2784	2785	5288	5289
673	2786	2787	5290	5291
674	2788	2789	5292	5293
675	2790	2791	5294	5295
676	2792	2793	5296	5297
677	2794	2795	5298	5299
678	2796	2797	5300	5301
679	2798	2799	5302	5303
680	2800	2801	5304	5305
681	2804	2805	5308	5309
682	2806	2807	5310	5311
683	2808	2809	5312	5313
684	2810	2811	5314	5315
685	2812	2813	5316	5317
686	2814	2815	5318	5319
687	2816	2817	5320	5321
688	2818	2819	5322	5323
689	2820	2821	5324	5325
690	2822	2823	5326	5327
691	2824	2825	5328	5329
692	2826	2827	5330	5331
693	2828	2829	5332	5333
694	2830	2831	5334	5335
695	2832	2833	5336	5337
696	2834	2835	5338	5339
697	2836	2837	5340	5341
698	2838	2839	5342	5343
699	2840	2841	5344	5345

700	2842	2843	5346	5347
701	2844	2845	5348	5349
702	2846	2847	5350	5351
703	2848	2849	5352	5353
704	2850	2851	5354	5355
705	2852	2853	5356	5357
706	2854	2855	5358	5359
707	2856	2857	5360	5361
708	2858	2859	5362	5363
709	2860	2861	5364	5365
710	2862	2863	5366	5367
711	2864	2865	5368	5369
712	2866	2867	5370	5371
713	2868	2869	5372	5373
714	2870	2871	5374	5375
715	2872	2873	5376	5377
716	2874	2875	5378	5379
717	2876	2877	5380	5381
718	2878	2879	5382	5383
719	2880	2881	5384	5385
720	2882	2883	5386	5387
721	2886	2887	5390	5391
722	2888	2889	5392	5393
723	2884	2885	5388	5389
724	2890	2891	5394	5395
725	2892	2893	5396	5397
726	2894	2895	5398	5399
727	2896	2897	5400	5401
728	2900	2901	5404	5405
729	2902	2903	5406	5407
730	2904	2905	5408	5409
731	2906	2907	5410	5411
732	2908	2909	5412	5413
733	2910	2911	5414	5415
734	2912	2913	5416	5417

735	2914	2915	5418	5419
736	2916	2917	5420	5421
737	2918	2919	5422	5423
738	2920	2921	5424	5425
739	2922	2923	5426	5427
740	2924	2925	5428	5429
741	2926	2927	5430	5431
742	2928	2929	5432	5433
743	2930	2931	5434	5435
744	2932	2933	5436	5437
745	2934	2935	5438	5439
746	2936	2937	5440	5441
747	2938	2939	5442	5443
748	2940	2941	5444	5445
749	2942	2943	5446	5447
750	2944	2945	5448	5449
751	2946	2947	5450	5451
752	2948	2949	5452	5453
753	2952	2953	5456	5457
754	2954	2955	5458	5459
755	2956	2957	5460	5461
756	2958	2959	5462	5463
757	2960	2961	5464	5465
758	2962	2963	5466	5467
759	2964	2965	5468	5469
760	2966	2967	5470	5471
761	2968	2969	5472	5473
762	2970	2971	5474	5475
763	2972	2973	5476	5477
764	2974	2975	5478	5479
765	2976	2977	5480	5481
766	2978	2979	5482	5483
767	2980	2981	5484	5485
768	2982	2983	5486	5487
769	2984	2985	5488	5489

770	2986	2987	5490	5491
771	2990	2991	5494	5495
772	2992	2993	5496	5497
773	2994	2995	5498	5499
774	2996	2997	5500	5501
775	2998	2999	5502	5503
776	3000	3001	5504	5505
777	3002	3003	5506	5507
778	3004	3005	5508	5509
779	3006	3007	5510	5511
780	3008	3009	5512	5513
781	3010	3011	5514	5515
782	3012	3013	5516	5517
783	3014	3015	5518	5519
784	3016	3017	5520	5521
785	3020	3021	5524	5525
786	3022	3023	5526	5527
787	3024	3025	5528	5529
788	3026	3027	5530	5531
789	3028	3029	5532	5533
790	3030	3031	5534	5535
791	3032	3033	5536	5537
792	3034	3035	5538	5539
793	3036	3037	5540	5541
794	3038	3039	5542	5543
795	3040	3041	5544	5545
796	3042	3043	5546	5547
797	3044	3045	5548	5549
798	3046	3047	5550	5551
799	3048	3049	5552	5553
800	3050	3051	5554	5555
801	3052	3053	5556	5557
802	3054	3055	5558	5559
803	3056	3057	5560	5561
804	3058	3059	5562	5563

805	3060	3061	5564	5565
806	3062	3063	5566	5567
807	3064	3065	5568	5569
808	3066	3067	5570	5571
809	3068	3069	5572	5573
810	3070	3071	5574	5575
811	3072	3073	5576	5577
812	3074	3075	5578	5579
813	3076	3077	5580	5581
814	3078	3079	5582	5583
815	3080	3081	5584	5585
816	3082	3083	5586	5587
817	3084	3085	5588	5589
818	3086	3087	5590	5591
819	3088	3089	5592	5593
820	3090	3091	5594	5595
821	3092	3093	5596	5597
822	3094	3095	5598	5599
823	3096	3097	5600	5601
824	3100	3101	5604	5605
825	3102	3103	5606	5607
826	3104	3105	5608	5609
827	3106	3107	5610	5611
828	3108	3109	5612	5613
829	3110	3111	5614	5615
830	3112	3113	5616	5617
831	3114	3115	5618	5619
832	3116	3117	5620	5621
833	3120	3121	5624	5625
834	3124	3125	5628	5629
835	3122	3123	5626	5627
836	3128	3129	5632	5633
837	3130	3131	5634	5635
838	3132	3133	5636	5637
839	3134	3135	5638	5639

840	3136	3137	5640	5641
841	3138	3139	5642	5643
842	3140	3141	5644	5645
843	3142	3143	5646	5647
844	3144	3145	5648	5649
845	3146	3147	5650	5651
846	3148	3149	5652	5653
847	3150	3151	5654	5655
848	3152	3153	5656	5657
849	3154	3155	5658	5659
850	3156	3157	5660	5661
851	3158	3159	5662	5663
852	3160	3161	5664	5665
853	3164	3165	5668	5669
854	3162	3163	5666	5667
855	3166	3167	5670	5671
856	3168	3169	5672	5673
857	3170	3171	5674	5675
858	3172	3173	5676	5677
859	3174	3175	5678	5679
860	3176	3177	5680	5681
861	3180	3181	5684	5685
862	3178	3179	5682	5683
863	3182	3183	5686	5687
864	3184	3185	5688	5689
865	3186	3187	5690	5691
866	3188	3189	5692	5693
867	3190	3191	5694	5695
868	3192	3193	5696	5697
869	3194	3195	5698	5699
870	3196	3197	5700	5701
871	3198	3199	5702	5703
872	3200	3201	5704	5705
873	3202	3203	5706	5707
874	3204	3205	5708	5709

875	3206	3207	5710	5711
876	3210	3211	5714	5715
877	3212	3213	5716	5717
878	3214	3215	5718	5719
879	3216	3217	5720	5721
880	3218	3219	5722	5723
881	3220	3221	5724	5725
882	3222	3223	5726	5727
883	3224	3225	5728	5729
884	3226	3227	5730	5731
885	3228	3229	5732	5733
886	3230	3231	5734	5735
887	3232	3233	5736	5737
888	3234	3235	5738	5739
889	3236	3237	5740	5741
890	3238	3239	5742	5743
891	3240	3241	5744	5745
892	3244	3245	5748	5749
893	3246	3247	5750	5751
894	3248	3249	5752	5753
895	3250	3251	5754	5755
896	3252	3253	5756	5757
897	3254	3255	5758	5759
898	3256	3257	5760	5761
899	3258	3259	5762	5763
900	3260	3261	5764	5765
901	3262	3263	5766	5767
902	3264	3265	5768	5769
903	3266	3267	5770	5771
904	3268	3269	5772	5773
905	3270	3271	5774	5775
906	3272	3273	5776	5777
907	3274	3275	5778	5779
908	3276	3277	5780	5781
909	3278	3279	5782	5783

910	3280	3281	5784	5785
911	3282	3283	5786	5787
912	3284	3285	5788	5789
913	3286	3287	5790	5791
914	3288	3289	5792	5793
915	3290	3291	5794	5795
916	3292	3293	5796	5797
917	3296	3297	5800	5801
918	3298	3299	5802	5803
919	3300	3301	5804	5805
920	3302	3303	5806	5807
921	3304	3305	5808	5809
922	3306	3307	5810	5811
923	3308	3309	5812	5813
924	3310	3311	5814	5815
925	3316	3317	5820	5821
926	3314	3315	5818	5819
927	3324	3325	5828	5829
928	3326	3327	5830	5831
929	3328	3329	5832	5833
930	3330	3331	5834	5835
931	3338	3339	5842	5843
932	3336	3337	5840	5841
933	3340	3341	5844	5845
934	3342	3343	5846	5847
935	3344	3345	5848	5849
936	3346	3347	5850	5851
937	3348	3349	5852	5853
938	3350	3351	5854	5855
939	3352	3353	5856	5857
940	3354	3355	5858	5859
941	3356	3357	5860	5861
942	3360	3361	5864	5865
943	3362	3363	5866	5867
944	3364	3365	5868	5869

945	3366	3367	5870	5871
946	3368	3369	5872	5873
947	3370	3371	5874	5875
948	3374	3375	5878	5879
949	3378	3379	5882	5883
950	3376	3377	5880	5881
951	3380	3381	5884	5885
952	3382	3383	5886	5887
953	3384	3385	5888	5889
954	3386	3387	5890	5891
955	3388	3389	5892	5893
956	3390	3391	5894	5895
957	3392	3393	5896	5897
958	3394	3395	5898	5899
959	3396	3397	5900	5901
960	3398	3399	5902	5903
961	3400	3401	5904	5905
962	3402	3403	5906	5907
963	3404	3405	5908	5909
964	3406	3407	5910	5911
965	3408	3409	5912	5913
966	3410	3411	5914	5915
967	3412	3413	5916	5917
968	3414	3415	5918	5919
969	3416	3417	5920	5921
970	3418	3419	5922	5923
971	3420	3421	5924	5925
972	3422	3423	5926	5927
973	3424	3425	5928	5929
974	3426	3427	5930	5931
975	3428	3429	5932	5933
976	3430	3431	5934	5935
977	3432	3433	5936	5937
978	3434	3435	5938	5939
979	3436	3437	5940	5941

980	3438	3439	5942	5943
981	3440	3441	5944	5945
982	3442	3443	5946	5947
983	3444	3445	5948	5949
984	3446	3447	5950	5951
985	3448	3449	5952	5953
986	3450	3451	5954	5955
987	3454	3455	5958	5959
988	3456	3457	5960	5961
989	3458	3459	5962	5963
990	3460	3461	5964	5965
991	3462	3463	5966	5967
992	3464	3465	5968	5969
993	3466	3467	5970	5971
994	3468	3469	5972	5973
995	3470	3471	5974	5975
996	3472	3473	5976	5977
997	3474	3475	5978	5979
998	3476	3477	5980	5981
999	3478	3479	5982	5983
1000	3480	3481	5984	5985
1001	3482	3483	5986	5987
1002	3484	3485	5988	5989
1003	3486	3487	5990	5991
1004	3488	3489	5992	5993
1005	3490	3491	5994	5995
1006	3494	3495	5998	5999
1007	3496	3497	6000	6001
1008	3498	3499	6002	6003
1009	3500	3501	6004	6005
1010	3502	3503	6006	6007
1011	3504	3505	6008	6009
1012	3506	3507	6010	6011
1013	3508	3509	6012	6013
1014	3510	3511	6014	6015

1015	3512	3513	6016	6017
1016	3516	3517	6020	6021
1017	3518	3519	6022	6023
1018	3520	3521	6024	6025
1019	3522	3523	6026	6027
1020	3524	3525	6028	6029
1021	3526	3527	6030	6031
1022	3528	3529	6032	6033
1023	3530	3531	6034	6035
1024	3532	3533	6036	6037
1025	3534	3535	6038	6039
1026	3536	3537	6040	6041
1027	3542	3543	6046	6047
1028	3544	3545	6048	6049
1029	3546	3547	6050	6051
1030	3548	3549	6052	6053
1031	3550	3551	6054	6055
1032	3552	3553	6056	6057
1033	3554	3555	6058	6059
1034	3556	3557	6060	6061
1035	3558	3559	6062	6063
1036	3560	3561	6064	6065
1037	3562	3563	6066	6067
1038	3564	3565	6068	6069
1039	3566	3567	6070	6071
1040	3568	3569	6072	6073
1041	3570	3571	6074	6075
1042	3572	3573	6076	6077
1043	3574	3575	6078	6079
1044	3582	3583	6086	6087
1045	3584	3585	6088	6089
1046	3586	3587	6090	6091
1047	3588	3589	6092	6093
1048	3592	3593	6096	6097
1049	3594	3595	6098	6099

1050	3596	3597	6100	6101
1051	3598	3599	6102	6103
1052	3600	3601	6104	6105
1053	3602	3603	6106	6107
1054	3604	3605	6108	6109
1055	3606	3607	6110	6111
1056	3608	3609	6112	6113
1057	3610	3611	6114	6115
1058	3612	3613	6116	6117
1059	3614	3615	6118	6119
1060	3616	3617	6120	6121
1061	3618	3619	6122	6123
1062	3620	3621	6124	6125
1063	3622	3623	6126	6127
1064	3624	3625	6128	6129
1065	3626	3627	6130	6131
1066	3628	3629	6132	6133
1067	3630	3631	6134	6135
1068	3632	3633	6136	6137
1069	3634	3635	6138	6139
1070	3636	3637	6140	6141
1071	3638	3639	6142	6143
1072	3640	3641	6144	6145
1073	3642	3643	6146	6147
1074	3644	3645	6148	6149
1075	3646	3647	6150	6151
1076	3648	3649	6152	6153
1077	3652	3653	6156	6157
1078	3654	3655	6158	6159
1079	3656	3657	6160	6161
1080	3658	3659	6162	6163
1081	3660	3661	6164	6165
1082	3662	3663	6166	6167
1083	3666	3667	6170	6171
1084	3668	3669	6172	6173

1085	3672	3673	6176	6177
1086	3674	3675	6178	6179
1087	3676	3677	6180	6181
1088	3678	3679	6182	6183
1089	3680	3681	6184	6185
1090	3682	3683	6186	6187
1091	3684	3685	6188	6189
1092	3686	3687	6190	6191
1093	3688	3689	6192	6193
1094	3690	3691	6194	6195
1095	3692	3693	6196	6197
1096	3694	3695	6198	6199
1097	3696	3697	6200	6201
1098	3698	3699	6202	6203
1099	3702	3703	6206	6207
1100	3700	3701	6204	6205
1101	3704	3705	6208	6209
1102	3706	3707	6210	6211
1103	3708	3709	6212	6213
1104	3714	3715	6218	6219
1105	3720	3721	6224	6225
1106	3722	3723	6226	6227
1107	3724	3725	6228	6229
1108	3726	3727	6230	6231
1109	3728	3729	6232	6233
1110	3730	3731	6234	6235
1111	3732	3733	6236	6237
1112	3734	3735	6238	6239
1113	3736	3737	6240	6241
1114	3740	3741	6244	6245
1115	3738	3739	6242	6243
1116	3742	3743	6246	6247
1117	3744	3745	6248	6249
1118	3746	3747	6250	6251
1119	3748	3749	6252	6253

1120	3750	3751	6254	6255
1121	3754	3755	6258	6259
1122	3756	3757	6260	6261
1123	3758	3759	6262	6263
1124	3760	3761	6264	6265
1125	3762	3763	6266	6267
1126	3766	3767	6270	6271
1127	3770	3771	6274	6275
1128	3772	3773	6276	6277
1129	3776	3777	6280	6281
1130	3774	3775	6278	6279
1131	3778	3779	6282	6283
1132	3780	3781	6284	6285
1133	3782	3783	6286	6287
1134	3784	3785	6288	6289
1135	3788	3789	6292	6293
1136	3786	3787	6290	6291
1137	3794	3795	6298	6299
1138	1372	1373	3876	3877
1139	1378	1379	3882	3883
1140	1384	1385	3888	3889
1141	1390	1391	3894	3895
1142	1408	1409	3912	3913
1143	1436	1437	3940	3941
1144	1442	1443	3946	3947
1145	1466	1467	3970	3971
1146	1474	1475	3978	3979
1147	1528	1529	4032	4033
1148	1560	1561	4064	4065
1149	1578	1579	4082	4083
1150	1600	1601	4104	4105
1151	1602	1603	4106	4107
1152	1608	1609	4112	4113
1153	1610	1611	4114	4115
1154	1654	1655	4158	4159

1155	1660	1661	4164	4165
1156	1680	1681	4184	4185
1157	1682	1683	4186	4187
1158	1692	1693	4196	4197
1159	1702	1703	4206	4207
1160	1706	1707	4210	4211
1161	1716	1717	4220	4221
1162	1718	1719	4222	4223
1163	1730	1731	4234	4235
1164	1748	1749	4252	4253
1165	1780	1781	4284	4285
1166	1794	1795	4298	4299
1167	1798	1799	4302	4303
1168	1814	1815	4318	4319
1169	1816	1817	4320	4321
1170	1820	1821	4324	4325
1171	1822	1823	4326	4327
1172	1830	1831	4334	4335
1173	1832	1833	4336	4337
1174	1838	1839	4342	4343
1175	1844	1845	4348	4349
1176	1870	1871	4374	4375
1177	1880	1881	4384	4385
1178	1882	1883	4386	4387
1179	1884	1885	4388	4389
1180	1932	1933	4436	4437
1181	1968	1969	4472	4473
1182	1982	1983	4486	4487
1183	2036	2037	4540	4541
1184	2086	2087	4590	4591
1185	2098	2099	4602	4603
1186	2126	2127	4630	4631
1187	2132	2133	4636	4637
1188	2166	2167	4670	4671
1189	2168	2169	4672	4673

1190	2184	2185	4688	4689
1191	2240	2241	4744	4745
1192	2276	2277	4780	4781
1193	2300	2301	4804	4805
1194	2302	2303	4806	4807
1195	2330	2331	4834	4835
1196	2336	2337	4840	4841
1197	2448	2449	4952	4953
1198	2452	2453	4956	4957
1199	2484	2485	4988	4989
1200	2512	2513	5016	5017
1201	2530	2531	5034	5035
1202	2540	2541	5044	5045
1203	2542	2543	5046	5047
1204	2584	2585	5088	5089
1205	2586	2587	5090	5091
1206	2588	2589	5092	5093
1207	2614	2615	5118	5119
1208	2670	2671	5174	5175
1209	2694	2695	5198	5199
1210	2708	2709	5212	5213
1211	2730	2731	5234	5235
1212	2734	2735	5238	5239
1213	2746	2747	5250	5251
1214	2802	2803	5306	5307
1215	2898	2899	5402	5403
1216	2950	2951	5454	5455
1217	2988	2989	5492	5493
1218	3018	3019	5522	5523
1219	3098	3099	5602	5603
1220	3118	3119	5622	5623
1221	3126	3127	5630	5631
1222	3208	3209	5712	5713
1223	3242	3243	5746	5747
1224	3294	3295	5798	5799

1225	3312	3313	5816	5817
1226	3318	3319	5822	5823
1227	3320	3321	5824	5825
1228	3322	3323	5826	5827
1229	3332	3333	5836	5837
1230	3334	3335	5838	5839
1231	3358	3359	5862	5863
1232	3372	3373	5876	5877
1233	3452	3453	5956	5957
1234	3492	3493	5996	5997
1235	3514	3515	6018	6019
1236	3538	3539	6042	6043
1237	3540	3541	6044	6045
1238	3576	3577	6080	6081
1239	3578	3579	6082	6083
1240	3580	3581	6084	6085
1241	3590	3591	6094	6095
1242	3650	3651	6154	6155
1243	3664	3665	6168	6169
1244	3670	3671	6174	6175
1245	3710	3711	6214	6215
1246	3712	3713	6216	6217
1247	3716	3717	6220	6221
1248	3718	3719	6222	6223
1249	3752	3753	6256	6257
1250	3764	3765	6268	6269
1251	3768	3769	6272	6273
1252	3790	3791	6294	6295
1253	3792	3793	6296	6297
1254	6300	6301	6376	6377
1255	6302	6303	6378	6379
1256	6304	6305	6380	6381
1257	6306	6307	6382	6383
1258	6308	6309	6384	6385
1259	6310	6311	6386	6387

1260	6312	6313	6388	6389
1261	6314	6315	6390	6391
1262	6316	6317	6392	6393
1263	6318	6319	6394	6395
1264	6320	6321	6396	6397
1265	6322	6323	6398	6399
1266	6324	6325	6400	6401
1267	6326	6327	6402	6403
1268	6328	6329	6404	6405
1269	6330	6331	6406	6407
1270	6332	6333	6408	6409
1271	6334	6335	6410	6411
1272	6336	6337	6412	6413
1273	6338	6339	6414	6415
1274	6340	6341	6416	6417
1275	6342	6343	6418	6419
1276	6344	6345	6420	6421
1277	6346	6347	6422	6423
1278	6348	6349	6424	6425
1279	6350	6351	6426	6427
1280	6352	6353	6428	6429
1281	6354	6355	6430	6431
1282	6356	6357	6432	6433
1283	6358	6359	6434	6435
1284	6360	6361	6436	6437
1285	6362	6363	6438	6439
1286	6364	6365	6440	6441
1287	6366	6367	6442	6443
1288	6368	6369	6444	6445
1289	6370	6371	6446	6447
1290	6372	6373	6448	6449
1291	6374	6375	6450	6451

TABLE 5

<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>
1292	F	1229848	3012	F	833844	4732	B	455875
1293	F	1227874	3013	F	831936	4733	B	457736
1294	F	1018	3014	F	834905	4734	B	457231
1295	F	1229162	3015	F	832943	4735	B	459146
1296	F	1588	3016	F	835834	4736	B	458008
1297	F	1229711	3017	F	833938	4737	B	459836
1298	F	2253	3018	F	837457	4738	B	458598
1299	F	369	3019	F	835536	4739	B	460488
1300	F	3381	3020	F	838723	4740	B	459717
1301	F	1508	3021	F	836826	4741	B	461652
1302	F	4042	3022	F	840649	4742	B	460417
1303	F	2126	3023	F	838723	4743	B	462365
1304	F	5735	3024	F	841751	4744	B	461391
1305	F	3843	3025	F	839825	4745	B	463286
1306	F	7832	3026	F	842960	4746	B	461680
1307	F	5909	3027	F	841123	4747	B	463584
1308	F	8887	3028	F	843765	4748	B	462520
1309	F	7010	3029	F	841844	4749	B	464418
1310	F	10139	3030	F	844768	4750	B	463584
1311	F	8175	3031	F	842852	4751	B	465539
1312	F	10640	3032	F	846089	4752	B	464547
1313	F	8799	3033	F	844175	4753	B	466398
1314	F	10997	3034	F	848293	4754	B	465288
1315	F	9037	3035	F	846449	4755	B	467243
1316	F	12458	3036	F	848867	4756	B	465835
1317	F	10572	3037	F	846964	4757	B	467738
1318	F	14187	3038	F	850351	4758	B	466558
1319	F	12365	3039	F	848426	4759	B	468474
1320	F	15529	3040	F	851788	4760	B	467322
1321	F	13629	3041	F	849899	4761	B	469217
1322	F	17626	3042	F	852166	4762	B	467738
1323	F	15699	3043	F	850278	4763	B	469637
1324	F	20909	3044	F	853976	4764	B	469912

1325	F	19006	3045	F	852069	4765	B	471814
1326	F	21800	3046	F	854899	4766	B	470920
1327	F	19927	3047	F	853006	4767	B	472826
1328	F	23462	3048	F	855595	4768	B	472075
1329	F	21557	3049	F	853679	4769	B	473922
1330	F	25637	3050	F	856479	4770	B	472231
1331	F	23729	3051	F	854582	4771	B	474144
1332	F	25997	3052	F	858498	4772	B	472579
1333	F	24071	3053	F	856492	4773	B	474501
1334	F	26727	3054	F	859372	4774	B	473751
1335	F	24828	3055	F	857424	4775	B	475664
1336	F	27528	3056	F	860050	4776	B	475116
1337	F	25628	3057	F	858116	4777	B	477009
1338	F	28643	3058	F	860941	4778	B	477566
1339	F	26765	3059	F	859023	4779	B	479490
1340	F	29202	3060	F	861464	4780	B	477851
1341	F	27313	3061	F	859572	4781	B	479753
1342	F	29793	3062	F	862749	4782	B	478728
1343	F	27835	3063	F	860895	4783	B	480616
1344	F	31488	3064	F	864599	4784	B	479496
1345	F	29639	3065	F	862683	4785	B	481418
1346	F	31957	3066	F	865003	4786	B	479928
1347	F	30050	3067	F	863040	4787	B	481844
1348	F	33570	3068	F	866331	4788	B	481674
1349	F	31666	3069	F	864443	4789	B	483578
1350	F	34564	3070	F	866799	4790	B	482281
1351	F	32664	3071	F	864889	4791	B	484243
1352	F	35783	3072	F	867574	4792	B	482820
1353	F	33875	3073	F	865664	4793	B	484721
1354	F	37597	3074	F	868402	4794	B	484449
1355	F	35741	3075	F	866513	4795	B	486360
1356	F	39135	3076	F	869823	4796	B	485499
1357	F	37236	3077	F	867898	4797	B	487293
1358	F	38939	3078	F	870414	4798	B	486116
1359	F	37038	3079	F	868478	4799	B	487980

1360	F	40872	3080	F	871862	4800	B	486811
1361	F	38972	3081	F	869956	4801	B	488721
1362	F	42825	3082	F	872261	4802	B	487217
1363	F	40923	3083	F	870367	4803	B	489101
1364	F	43563	3084	F	874062	4804	B	487567
1365	F	41652	3085	F	872141	4805	B	489423
1366	F	44531	3086	F	874363	4806	B	487984
1367	F	42623	3087	F	872439	4807	B	489909
1368	F	45150	3088	F	875155	4808	B	489291
1369	F	43250	3089	F	873244	4809	B	491191
1370	F	45478	3090	F	878156	4810	B	489561
1371	F	43579	3091	F	876291	4811	B	491461
1372	F	46755	3092	F	879046	4812	B	490221
1373	F	44874	3093	F	877133	4813	B	492078
1374	F	47347	3094	F	880361	4814	B	490773
1375	F	45386	3095	F	878450	4815	B	492672
1376	F	47818	3096	F	882361	4816	B	491383
1377	F	45897	3097	F	880493	4817	B	493293
1378	F	48893	3098	F	883067	4818	B	491616
1379	F	46995	3099	F	881185	4819	B	493537
1380	F	49907	3100	F	883310	4820	B	492362
1381	F	48000	3101	F	881416	4821	B	494246
1382	F	51088	3102	F	884035	4822	B	495083
1383	F	49169	3103	F	882152	4823	B	497027
1384	F	52651	3104	F	885495	4824	B	496168
1385	F	50721	3105	F	883599	4825	B	498063
1386	F	53065	3106	F	887340	4826	B	496789
1387	F	51176	3107	F	885448	4827	B	498688
1388	F	53516	3108	F	887996	4828	B	497500
1389	F	51611	3109	F	886093	4829	B	499390
1390	F	54242	3110	F	888494	4830	B	498057
1391	F	52351	3111	F	886570	4831	B	499966
1392	F	55058	3112	F	889100	4832	B	498552
1393	F	53159	3113	F	887201	4833	B	500508
1394	F	56274	3114	F	889655	4834	B	499240

1395	F	54348	3115	F	887776	4835	B	501145
1396	F	57078	3116	F	891025	4836	B	499812
1397	F	55156	3117	F	889105	4837	B	501762
1398	F	58343	3118	F	891504	4838	B	500020
1399	F	56392	3119	F	889593	4839	B	501915
1400	F	61103	3120	F	891795	4840	B	500716
1401	F	59177	3121	F	889841	4841	B	502628
1402	F	59701	3122	F	892279	4842	B	504395
1403	F	57802	3123	F	890400	4843	B	506292
1404	F	61887	3124	F	892182	4844	B	504885
1405	F	59971	3125	F	890288	4845	B	506772
1406	F	62255	3126	F	893010	4846	B	507107
1407	F	60348	3127	F	891139	4847	B	509003
1408	F	63515	3128	F	893101	4848	B	507933
1409	F	61557	3129	F	891211	4849	B	509795
1410	F	63657	3130	F	895494	4850	B	510741
1411	F	61761	3131	F	893599	4851	B	512656
1412	F	64088	3132	F	896448	4852	B	508573
1413	F	62196	3133	F	894511	4853	B	510445
1414	F	64422	3134	F	897341	4854	B	513663
1415	F	62537	3135	F	895442	4855	B	515585
1416	F	65072	3136	F	899197	4856	B	515276
1417	F	63140	3137	F	897279	4857	B	517040
1418	F	65978	3138	F	899999	4858	B	517602
1419	F	64088	3139	F	898075	4859	B	519510
1420	F	67046	3140	F	903008	4860	B	517602
1421	F	65146	3141	F	901103	4861	B	519510
1422	F	67466	3142	F	904798	4862	B	518075
1423	F	65580	3143	F	902923	4863	B	519947
1424	F	68569	3144	F	906993	4864	B	518429
1425	F	66686	3145	F	905129	4865	B	520326
1426	F	68609	3146	F	907564	4866	B	521416
1427	F	66688	3147	F	905665	4867	B	523319
1428	F	70423	3148	F	907913	4868	B	523196
1429	F	68479	3149	F	905998	4869	B	525096

1430	F	71099	3150	F	908349	4870	B	525033
1431	F	69206	3151	F	906425	4871	B	526939
1432	F	71829	3152	F	909186	4872	B	524599
1433	F	69935	3153	F	907286	4873	B	526501
1434	F	73745	3154	F	911413	4874	B	526494
1435	F	71931	3155	F	909481	4875	B	528361
1436	F	76942	3156	F	912084	4876	B	527330
1437	F	75022	3157	F	910176	4877	B	529238
1438	F	77404	3158	F	912718	4878	B	527167
1439	F	75556	3159	F	910814	4879	B	529067
1440	F	78133	3160	F	913813	4880	B	528673
1441	F	76192	3161	F	911941	4881	B	530573
1442	F	79079	3162	F	915106	4882	B	529456
1443	F	77122	3163	F	913211	4883	B	531376
1444	F	79471	3164	F	915053	4884	B	530864
1445	F	77481	3165	F	913141	4885	B	532745
1446	F	79670	3166	F	916630	4886	B	531906
1447	F	77816	3167	F	914731	4887	B	533776
1448	F	80236	3168	F	917500	4888	B	534199
1449	F	78356	3169	F	915594	4889	B	536103
1450	F	81108	3170	F	918615	4890	B	536674
1451	F	79182	3171	F	916715	4891	B	538552
1452	F	83024	3172	F	919639	4892	B	537422
1453	F	81158	3173	F	917732	4893	B	539270
1454	F	83786	3174	F	920216	4894	B	538165
1455	F	81886	3175	F	918312	4895	B	540048
1456	F	84739	3176	F	920971	4896	B	538658
1457	F	82821	3177	F	919057	4897	B	540578
1458	F	84866	3178	F	921889	4898	B	538970
1459	F	82967	3179	F	920015	4899	B	540857
1460	F	85175	3180	F	921773	4900	B	539859
1461	F	83240	3181	F	919871	4901	B	541736
1462	F	85690	3182	F	923428	4902	B	541474
1463	F	83790	3183	F	921546	4903	B	543411
1464	F	86397	3184	F	923841	4904	B	542791

1465	F	84507	3185	F	921936	4905	B	544691
1466	F	88470	3186	F	924795	4906	B	543234
1467	F	86563	3187	F	922945	4907	B	545134
1468	F	89038	3188	F	925102	4908	B	543608
1469	F	87121	3189	F	923188	4909	B	545513
1470	F	91017	3190	F	926130	4910	B	546851
1471	F	89146	3191	F	924248	4911	B	548762
1472	F	93075	3192	F	927729	4912	B	549793
1473	F	91147	3193	F	925829	4913	B	551652
1474	F	93846	3194	F	928112	4914	B	547523
1475	F	91948	3195	F	926130	4915	B	549430
1476	F	94410	3196	F	929014	4916	B	550754
1477	F	92561	3197	F	927129	4917	B	552702
1478	F	95447	3198	F	930776	4918	B	551775
1479	F	93541	3199	F	928876	4919	B	553674
1480	F	96074	3200	F	931898	4920	B	552876
1481	F	94197	3201	F	929987	4921	B	554756
1482	F	97706	3202	F	932291	4922	B	555340
1483	F	95841	3203	F	930323	4923	B	557240
1484	F	98142	3204	F	933264	4924	B	555736
1485	F	96292	3205	F	931339	4925	B	557619
1486	F	99925	3206	F	935505	4926	B	558229
1487	F	98011	3207	F	933605	4927	B	560135
1488	F	101229	3208	F	936779	4928	B	558821
1489	F	99338	3209	F	934873	4929	B	560696
1490	F	101429	3210	F	937000	4930	B	559955
1491	F	99552	3211	F	935108	4931	B	561816
1492	F	102137	3212	F	938062	4932	B	561979
1493	F	100237	3213	F	936162	4933	B	563858
1494	F	102600	3214	F	938536	4934	B	561979
1495	F	100657	3215	F	936689	4935	B	563812
1496	F	103330	3216	F	938934	4936	B	564167
1497	F	101429	3217	F	937000	4937	B	566081
1498	F	103877	3218	F	939541	4938	B	565229
1499	F	101966	3219	F	937640	4939	B	567096

1500	F	104336	3220	F	940603	4940	B	566419
1501	F	102469	3221	F	938681	4941	B	568318
1502	F	108182	3222	F	940758	4942	B	567974
1503	F	106280	3223	F	938826	4943	B	569872
1504	F	111814	3224	F	941387	4944	B	568753
1505	F	109911	3225	F	939470	4945	B	570655
1506	F	112412	3226	F	942261	4946	B	569707
1507	F	110553	3227	F	940373	4947	B	571605
1508	F	113442	3228	F	942563	4948	B	571285
1509	F	111571	3229	F	940654	4949	B	573207
1510	F	113891	3230	F	942807	4950	B	572080
1511	F	112010	3231	F	940907	4951	B	573948
1512	F	114990	3232	F	943510	4952	B	572628
1513	F	113112	3233	F	941608	4953	B	574524
1514	F	115684	3234	F	943771	4954	B	573563
1515	F	113776	3235	F	941872	4955	B	575436
1516	F	116526	3236	F	944330	4956	B	572628
1517	F	114656	3237	F	942413	4957	B	574524
1518	F	117731	3238	F	945147	4958	B	575279
1519	F	115825	3239	F	943262	4959	B	577202
1520	F	118292	3240	F	945527	4960	B	576190
1521	F	116389	3241	F	943620	4961	B	578039
1522	F	119593	3242	F	946627	4962	B	578174
1523	F	117685	3243	F	944741	4963	B	580011
1524	F	120231	3244	F	947165	4964	B	579148
1525	F	118292	3245	F	945278	4965	B	581040
1526	F	122278	3246	F	948674	4966	B	580227
1527	F	120382	3247	F	946774	4967	B	582047
1528	F	122610	3248	F	949646	4968	B	580656
1529	F	120682	3249	F	947716	4969	B	582542
1530	F	123309	3250	F	950731	4970	B	580420
1531	F	121390	3251	F	948837	4971	B	582322
1532	F	126113	3252	F	951418	4972	B	581322
1533	F	124213	3253	F	949545	4973	B	583212
1534	F	128975	3254	F	951940	4974	B	582051

1535	F	127091	3255	F	950034	4975	B	583973
1536	F	134603	3256	F	952365	4976	B	582592
1537	F	132806	3257	F	950461	4977	B	584513
1538	F	136249	3258	F	953230	4978	B	583651
1539	F	134352	3259	F	951316	4979	B	585588
1540	F	137680	3260	F	954978	4980	B	584932
1541	F	135756	3261	F	953125	4981	B	586813
1542	F	137680	3262	F	955613	4982	B	585457
1543	F	135799	3263	F	953697	4983	B	587360
1544	F	138035	3264	F	956989	4984	B	587145
1545	F	136135	3265	F	955136	4985	B	589063
1546	F	139266	3266	F	957684	4986	B	588150
1547	F	137363	3267	F	955778	4987	B	590044
1548	F	140208	3268	F	959156	4988	B	588404
1549	F	138351	3269	F	957187	4989	B	590304
1550	F	141636	3270	F	960035	4990	B	589320
1551	F	139735	3271	F	958117	4991	B	591193
1552	F	142808	3272	F	961584	4992	B	590733
1553	F	140900	3273	F	959727	4993	B	592677
1554	F	144272	3274	F	965172	4994	B	592682
1555	F	142372	3275	F	963269	4995	B	594583
1556	F	145217	3276	F	966747	4996	B	593126
1557	F	143335	3277	F	964843	4997	B	595026
1558	F	146527	3278	F	968015	4998	B	594005
1559	F	144645	3279	F	966111	4999	B	595882
1560	F	146965	3280	F	968508	5000	B	594521
1561	F	145086	3281	F	966609	5001	B	596421
1562	F	147455	3282	F	969289	5002	B	596170
1563	F	145501	3283	F	967389	5003	B	598096
1564	F	148810	3284	F	969537	5004	B	596532
1565	F	146904	3285	F	967640	5005	B	598451
1566	F	151964	3286	F	970078	5006	B	597438
1567	F	150062	3287	F	968137	5007	B	599365
1568	F	154064	3288	F	970317	5008	B	598191
1569	F	152113	3289	F	968394	5009	B	600088

1570	F	154888	3290	F	970857	5010	B	598836
1571	F	152963	3291	F	968969	5011	B	600749
1572	F	155418	3292	F	971657	5012	B	599476
1573	F	153558	3293	F	969757	5013	B	601327
1574	F	156528	3294	F	974954	5014	B	600192
1575	F	154606	3295	F	973067	5015	B	602103
1576	F	157433	3296	F	975200	5016	B	601131
1577	F	155516	3297	F	973300	5017	B	603030
1578	F	158771	3298	F	976362	5018	B	602307
1579	F	156842	3299	F	974418	5019	B	604209
1580	F	159105	3300	F	977009	5020	B	602810
1581	F	157219	3301	F	975050	5021	B	604759
1582	F	159657	3302	F	978153	5022	B	603529
1583	F	157761	3303	F	976255	5023	B	605402
1584	F	160240	3304	F	980532	5024	B	604759
1585	F	158316	3305	F	978632	5025	B	606662
1586	F	160675	3306	F	981701	5026	B	606076
1587	F	158778	3307	F	979785	5027	B	608046
1588	F	161289	3308	F	982885	5028	B	606843
1589	F	159402	3309	F	980983	5029	B	608746
1590	F	161918	3310	F	983878	5030	B	607504
1591	F	159979	3311	F	981973	5031	B	609404
1592	F	162214	3312	F	985264	5032	B	609224
1593	F	160297	3313	F	983395	5033	B	611138
1594	F	163996	3314	F	986953	5034	B	609952
1595	F	162045	3315	F	985049	5035	B	611865
1596	F	165189	3316	F	985623	5036	B	611138
1597	F	163288	3317	F	983760	5037	B	613033
1598	F	166730	3318	F	986956	5038	B	612012
1599	F	164828	3319	F	985049	5039	B	613917
1600	F	168243	3320	F	987506	5040	B	612554
1601	F	166327	3321	F	985592	5041	B	614453
1602	F	168907	3322	F	988307	5042	B	614136
1603	F	167064	3323	F	986404	5043	B	616017
1604	F	169129	3324	F	988783	5044	B	614978

1605	F	167294	3325	F	986927	5045	B	616936
1606	F	170632	3326	F	989593	5046	B	615399
1607	F	168692	3327	F	987694	5047	B	617342
1608	F	171229	3328	F	990733	5048	B	616565
1609	F	169381	3329	F	988783	5049	B	618402
1610	F	171553	3330	F	991559	5050	B	617618
1611	F	169614	3331	F	989675	5051	B	619515
1612	F	172433	3332	F	992323	5052	B	619027
1613	F	170533	3333	F	990421	5053	B	620937
1614	F	173217	3334	F	992522	5054	B	620142
1615	F	171316	3335	F	990640	5055	B	622052
1616	F	174567	3336	F	993308	5056	B	620230
1617	F	172680	3337	F	991361	5057	B	622124
1618	F	175342	3338	F	992795	5058	B	621498
1619	F	173479	3339	F	990919	5059	B	623385
1620	F	175709	3340	F	994573	5060	B	622583
1621	F	173752	3341	F	992673	5061	B	624479
1622	F	176909	3342	F	995517	5062	B	623718
1623	F	175009	3343	F	993570	5063	B	625598
1624	F	176704	3344	F	996518	5064	B	624533
1625	F	174761	3345	F	994660	5065	B	626462
1626	F	177608	3346	F	997317	5066	B	625020
1627	F	175709	3347	F	995450	5067	B	626893
1628	F	179259	3348	F	998653	5068	B	625774
1629	F	177384	3349	F	996762	5069	B	627660
1630	F	179719	3350	F	999865	5070	B	626146
1631	F	177800	3351	F	997908	5071	B	628010
1632	F	181629	3352	F	1001112	5072	B	626646
1633	F	179743	3353	F	999238	5073	B	628522
1634	F	182851	3354	F	1001651	5074	B	628020
1635	F	180952	3355	F	999731	5075	B	629982
1636	F	184230	3356	F	1003237	5076	B	628882
1637	F	182335	3357	F	1001317	5077	B	630730
1638	F	184870	3358	F	1004049	5078	B	629982
1639	F	182962	3359	F	1002132	5079	B	631822

1640	F	185241	3360	F	1004252	5080	B	631862
1641	F	183348	3361	F	1002307	5081	B	633762
1642	F	185611	3362	F	1005400	5082	B	633774
1643	F	183685	3363	F	1003518	5083	B	635675
1644	F	186336	3364	F	1005892	5084	B	637192
1645	F	184445	3365	F	1003958	5085	B	639082
1646	F	188059	3366	F	1006516	5086	B	638321
1647	F	186171	3367	F	1004599	5087	B	640221
1648	F	190828	3368	F	1007332	5088	B	639082
1649	F	188956	3369	F	1005446	5089	B	640954
1650	F	191294	3370	F	1009066	5090	B	639317
1651	F	189428	3371	F	1007190	5091	B	641243
1652	F	192686	3372	F	1014072	5092	B	639860
1653	F	190788	3373	F	1012172	5093	B	641780
1654	F	193380	3374	F	1015614	5094	B	640868
1655	F	191474	3375	F	1013733	5095	B	642770
1656	F	193388	3376	F	1016078	5096	B	641243
1657	F	191474	3377	F	1014172	5097	B	643106
1658	F	193977	3378	F	1015924	5098	B	641605
1659	F	192059	3379	F	1014059	5099	B	643503
1660	F	195480	3380	F	1016230	5100	B	642538
1661	F	193585	3381	F	1014330	5101	B	644407
1662	F	195868	3382	F	1017479	5102	B	643243
1663	F	193969	3383	F	1015558	5103	B	645145
1664	F	197913	3384	F	1018915	5104	B	643550
1665	F	196013	3385	F	1017003	5105	B	645450
1666	F	199088	3386	F	1019328	5106	B	643925
1667	F	197213	3387	F	1017440	5107	B	645837
1668	F	202776	3388	F	1020813	5108	B	645848
1669	F	200876	3389	F	1018915	5109	B	647759
1670	F	204467	3390	F	1021621	5110	B	645987
1671	F	202497	3391	F	1019671	5111	B	647969
1672	F	205584	3392	F	1023996	5112	B	646490
1673	F	203664	3393	F	1022107	5113	B	648429
1674	F	206940	3394	F	1024277	5114	B	646973

1675	F	205063	3395	F	1022385	5115	B	648871
1676	F	207560	3396	F	1025368	5116	B	648115
1677	F	205587	3397	F	1023468	5117	B	650007
1678	F	208048	3398	F	1026671	5118	B	648516
1679	F	206139	3399	F	1024821	5119	B	650374
1680	F	209923	3400	F	1027688	5120	B	650567
1681	F	208023	3401	F	1025823	5121	B	652472
1682	F	210455	3402	F	1030916	5122	B	651251
1683	F	208569	3403	F	1029047	5123	B	653140
1684	F	211049	3404	F	1031342	5124	B	653186
1685	F	209147	3405	F	1029430	5125	B	655076
1686	F	211596	3406	F	1032795	5126	B	653628
1687	F	209705	3407	F	1030916	5127	B	655515
1688	F	212226	3408	F	1032978	5128	B	656010
1689	F	210311	3409	F	1031078	5129	B	657870
1690	F	213832	3410	F	1033730	5130	B	656761
1691	F	211960	3411	F	1031839	5131	B	658636
1692	F	214866	3412	F	1035774	5132	B	658389
1693	F	212921	3413	F	1033821	5133	B	660295
1694	F	215173	3414	F	1036884	5134	B	660436
1695	F	213307	3415	F	1034954	5135	B	662352
1696	F	215800	3416	F	1037476	5136	B	663483
1697	F	213957	3417	F	1035577	5137	B	665358
1698	F	216489	3418	F	1037714	5138	B	664701
1699	F	214549	3419	F	1035847	5139	B	666607
1700	F	216980	3420	F	1038782	5140	B	665978
1701	F	215100	3421	F	1036884	5141	B	667856
1702	F	217665	3422	F	1040777	5142	B	667238
1703	F	215793	3423	F	1038856	5143	B	669172
1704	F	218039	3424	F	1042132	5144	B	668195
1705	F	216071	3425	F	1040216	5145	B	670046
1706	F	218476	3426	F	1043148	5146	B	668791
1707	F	216560	3427	F	1041215	5147	B	670691
1708	F	218769	3428	F	1044388	5148	B	669426
1709	F	216809	3429	F	1042445	5149	B	671326

1710	F	220020	3430	F	1045164	5150	B	671116
1711	F	218128	3431	F	1043224	5151	B	673055
1712	F	221210	3432	F	1046223	5152	B	671659
1713	F	219275	3433	F	1044324	5153	B	673547
1714	F	222497	3434	F	1047299	5154	B	672474
1715	F	220601	3435	F	1045364	5155	B	674347
1716	F	223292	3436	F	1049803	5156	B	673238
1717	F	221403	3437	F	1047914	5157	B	675140
1718	F	223775	3438	F	1050341	5158	B	674944
1719	F	221877	3439	F	1048431	5159	B	676911
1720	F	224250	3440	F	1050862	5160	B	674797
1721	F	222377	3441	F	1048907	5161	B	676669
1722	F	224906	3442	F	1051515	5162	B	675741
1723	F	223008	3443	F	1049572	5163	B	677643
1724	F	225283	3444	F	1051828	5164	B	676340
1725	F	223418	3445	F	1049917	5165	B	678204
1726	F	226670	3446	F	1052885	5166	B	676911
1727	F	224770	3447	F	1050957	5167	B	678770
1728	F	227849	3448	F	1053963	5168	B	677240
1729	F	225937	3449	F	1052057	5169	B	679136
1730	F	228185	3450	F	1055238	5170	B	677873
1731	F	226269	3451	F	1053362	5171	B	679767
1732	F	228393	3452	F	1055849	5172	B	678549
1733	F	226512	3453	F	1053963	5173	B	680420
1734	F	229334	3454	F	1056332	5174	B	679692
1735	F	227499	3455	F	1054465	5175	B	681628
1736	F	230761	3456	F	1056738	5176	B	680320
1737	F	228846	3457	F	1054830	5177	B	682220
1738	F	231287	3458	F	1058019	5178	B	681126
1739	F	229334	3459	F	1056110	5179	B	683046
1740	F	231731	3460	F	1058504	5180	B	682558
1741	F	229927	3461	F	1056587	5181	B	684404
1742	F	232865	3462	F	1059300	5182	B	681857
1743	F	231027	3463	F	1057406	5183	B	683768
1744	F	232865	3464	F	1060356	5184	B	683046

1745	F	231027	3465	F	1058400	5185	B	684944
1746	F	234315	3466	F	1061455	5186	B	684128
1747	F	232394	3467	F	1059456	5187	B	686124
1748	F	234823	3468	F	1062092	5188	B	684893
1749	F	232865	3469	F	1060243	5189	B	686740
1750	F	235154	3470	F	1063884	5190	B	685389
1751	F	233245	3471	F	1061983	5191	B	687290
1752	F	236429	3472	F	1064928	5192	B	686207
1753	F	234520	3473	F	1063056	5193	B	688106
1754	F	237268	3474	F	1067125	5194	B	687534
1755	F	235271	3475	F	1065240	5195	B	689424
1756	F	238047	3476	F	1067963	5196	B	688416
1757	F	236162	3477	F	1066075	5197	B	690275
1758	F	238636	3478	F	1068596	5198	B	688955
1759	F	236736	3479	F	1066668	5199	B	690855
1760	F	239957	3480	F	1069752	5200	B	689727
1761	F	238047	3481	F	1067890	5201	B	691626
1762	F	241373	3482	F	1071068	5202	B	690496
1763	F	239482	3483	F	1069210	5203	B	692386
1764	F	242017	3484	F	1072701	5204	B	691349
1765	F	240072	3485	F	1070806	5205	B	693249
1766	F	242740	3486	F	1073987	5206	B	692864
1767	F	240829	3487	F	1072090	5207	B	694724
1768	F	243281	3488	F	1075643	5208	B	695287
1769	F	241373	3489	F	1073742	5209	B	697187
1770	F	244244	3490	F	1076350	5210	B	696275
1771	F	242345	3491	F	1074450	5211	B	698172
1772	F	246052	3492	F	1077354	5212	B	696786
1773	F	244179	3493	F	1075555	5213	B	698696
1774	F	247581	3494	F	1077778	5214	B	698185
1775	F	245697	3495	F	1075880	5215	B	700090
1776	F	249216	3496	F	1078445	5216	B	700037
1777	F	247244	3497	F	1076529	5217	B	701923
1778	F	251003	3498	F	1079373	5218	B	702172
1779	F	249137	3499	F	1077523	5219	B	704050

1780	F	252064	3500	F	1079715	5220	B	703443
1781	F	250189	3501	F	1077850	5221	B	705316
1782	F	252900	3502	F	1080538	5222	B	704441
1783	F	251000	3503	F	1078655	5223	B	706351
1784	F	253718	3504	F	1081108	5224	B	705516
1785	F	251855	3505	F	1079228	5225	B	707413
1786	F	254993	3506	F	1083006	5226	B	706312
1787	F	253138	3507	F	1081108	5227	B	708190
1788	F	256414	3508	F	1084404	5228	B	707058
1789	F	254509	3509	F	1082465	5229	B	708979
1790	F	257283	3510	F	1085896	5230	B	707856
1791	F	255383	3511	F	1083990	5231	B	709719
1792	F	257279	3512	F	1086468	5232	B	708906
1793	F	255379	3513	F	1084563	5233	B	710811
1794	F	258061	3514	F	1087889	5234	B	709258
1795	F	256107	3515	F	1085985	5235	B	711132
1796	F	259005	3516	F	1088427	5236	B	710074
1797	F	257128	3517	F	1086527	5237	B	711924
1798	F	261075	3518	F	1088927	5238	B	710328
1799	F	259195	3519	F	1087027	5239	B	712212
1800	F	261551	3520	F	1089668	5240	B	711748
1801	F	259650	3521	F	1087768	5241	B	713690
1802	F	262535	3522	F	1092655	5242	B	712456
1803	F	260611	3523	F	1090767	5243	B	714407
1804	F	262960	3524	F	1093357	5244	B	715001
1805	F	261060	3525	F	1091465	5245	B	716854
1806	F	264509	3526	F	1093957	5246	B	715983
1807	F	262614	3527	F	1092070	5247	B	717887
1808	F	265837	3528	F	1095818	5248	B	717800
1809	F	263925	3529	F	1093955	5249	B	719668
1810	F	266239	3530	F	1096359	5250	B	718468
1811	F	264367	3531	F	1094509	5251	B	720383
1812	F	267185	3532	F	1097047	5252	B	720469
1813	F	265286	3533	F	1095114	5253	B	722367
1814	F	267909	3534	F	1097365	5254	B	722645

1815	F	266037	3535	F	1095498	5255	B	724559
1816	F	268594	3536	F	1097646	5256	B	723280
1817	F	266756	3537	F	1095767	5257	B	725273
1818	F	269299	3538	F	1098161	5258	B	723775
1819	F	267505	3539	F	1096242	5259	B	725691
1820	F	271044	3540	F	1098560	5260	B	724469
1821	F	269121	3541	F	1096663	5261	B	726387
1822	F	271737	3542	F	1099044	5262	B	725016
1823	F	269838	3543	F	1097150	5263	B	726902
1824	F	272558	3544	F	1099454	5264	B	726088
1825	F	270645	3545	F	1097547	5265	B	727988
1826	F	273007	3546	F	1100878	5266	B	727397
1827	F	271098	3547	F	1098942	5267	B	729236
1828	F	273463	3548	F	1101839	5268	B	728347
1829	F	271500	3549	F	1099956	5269	B	730278
1830	F	273922	3550	F	1104621	5270	B	728816
1831	F	272057	3551	F	1102789	5271	B	730718
1832	F	275083	3552	F	1106487	5272	B	729846
1833	F	273094	3553	F	1104562	5273	B	731740
1834	F	275495	3554	F	1107225	5274	B	730005
1835	F	273554	3555	F	1105318	5275	B	731898
1836	F	275739	3556	F	1107814	5276	B	730377
1837	F	273878	3557	F	1105922	5277	B	732272
1838	F	276229	3558	F	1108282	5278	B	730759
1839	F	274371	3559	F	1106374	5279	B	732659
1840	F	276548	3560	F	1113162	5280	B	732249
1841	F	274638	3561	F	1111308	5281	B	734124
1842	F	277098	3562	F	1114813	5282	B	732647
1843	F	275178	3563	F	1112949	5283	B	734590
1844	F	277358	3564	F	1116611	5284	B	733144
1845	F	275448	3565	F	1114766	5285	B	735088
1846	F	277609	3566	F	1118605	5286	B	733858
1847	F	275739	3567	F	1116725	5287	B	735787
1848	F	278314	3568	F	1119754	5288	B	734124
1849	F	276386	3569	F	1117874	5289	B	736028

1850	F	279310	3570	F	1120291	5290	B	734523
1851	F	277385	3571	F	1118385	5291	B	736441
1852	F	280627	3572	F	1121099	5292	B	735088
1853	F	278702	3573	F	1119202	5293	B	736978
1854	F	281471	3574	F	1121886	5294	B	735416
1855	F	279559	3575	F	1119982	5295	B	737315
1856	F	282239	3576	F	1122979	5296	B	735822
1857	F	280288	3577	F	1121038	5297	B	737700
1858	F	283832	3578	F	1123376	5298	B	736099
1859	F	281933	3579	F	1121486	5299	B	737981
1860	F	284384	3580	F	1124136	5300	B	736714
1861	F	282486	3581	F	1122333	5301	B	738612
1862	F	285373	3582	F	1124623	5302	B	737448
1863	F	283473	3583	F	1122723	5303	B	739321
1864	F	285919	3584	F	1125306	5304	B	737802
1865	F	284059	3585	F	1123423	5305	B	739693
1866	F	286742	3586	F	1126300	5306	B	738048
1867	F	284879	3587	F	1124399	5307	B	739948
1868	F	287216	3588	F	1127440	5308	B	738964
1869	F	285329	3589	F	1125545	5309	B	740808
1870	F	287671	3590	F	1128968	5310	B	739282
1871	F	285751	3591	F	1127134	5311	B	741190
1872	F	288273	3592	F	1129916	5312	B	739956
1873	F	286323	3593	F	1128111	5313	B	741906
1874	F	288618	3594	F	1131255	5314	B	740743
1875	F	286685	3595	F	1129330	5315	B	742597
1876	F	288273	3596	F	1132598	5316	B	741190
1877	F	286323	3597	F	1130684	5317	B	743081
1878	F	289723	3598	F	1133896	5318	B	741942
1879	F	287836	3599	F	1132002	5319	B	743875
1880	F	289508	3600	F	1134373	5320	B	743009
1881	F	287667	3601	F	1132510	5321	B	744914
1882	F	290750	3602	F	1135431	5322	B	743875
1883	F	288858	3603	F	1133531	5323	B	745738
1884	F	291142	3604	F	1135730	5324	B	744325

1885	F	289253	3605	F	1133823	5325	B	746234
1886	F	291702	3606	F	1136932	5326	B	744824
1887	F	289812	3607	F	1135040	5327	B	746724
1888	F	292522	3608	F	1139875	5328	B	745207
1889	F	290633	3609	F	1137942	5329	B	747073
1890	F	293035	3610	F	1141133	5330	B	746828
1891	F	291142	3611	F	1139231	5331	B	748738
1892	F	293731	3612	F	1142301	5332	B	747344
1893	F	291786	3613	F	1140366	5333	B	749206
1894	F	294530	3614	F	1145346	5334	B	748253
1895	F	292670	3615	F	1143505	5335	B	750094
1896	F	294367	3616	F	1146637	5336	B	748856
1897	F	292513	3617	F	1144743	5337	B	750717
1898	F	296092	3618	F	1147417	5338	B	749376
1899	F	294209	3619	F	1145547	5339	B	751265
1900	F	297611	3620	F	1147981	5340	B	750180
1901	F	295757	3621	F	1146086	5341	B	752086
1902	F	298027	3622	F	1148126	5342	B	750667
1903	F	296092	3623	F	1146211	5343	B	752569
1904	F	298555	3624	F	1148913	5344	B	751458
1905	F	296582	3625	F	1147044	5345	B	753343
1906	F	299403	3626	F	1149702	5346	B	753262
1907	F	297511	3627	F	1147890	5347	B	755162
1908	F	300409	3628	F	1150561	5348	B	754535
1909	F	298579	3629	F	1148660	5349	B	756429
1910	F	301332	3630	F	1150946	5350	B	756398
1911	F	299433	3631	F	1149046	5351	B	758298
1912	F	302215	3632	F	1152302	5352	B	756708
1913	F	300282	3633	F	1150392	5353	B	758611
1914	F	302492	3634	F	1154344	5354	B	760465
1915	F	300618	3635	F	1152371	5355	B	762358
1916	F	303627	3636	F	1155448	5356	B	761441
1917	F	301730	3637	F	1153548	5357	B	763356
1918	F	304350	3638	F	1156630	5358	B	762077
1919	F	302487	3639	F	1154729	5359	B	763945

1920	F	305173	3640	F	1157756	5360	B	762528
1921	F	303226	3641	F	1155862	5361	B	764410
1922	F	306244	3642	F	1160695	5362	B	763118
1923	F	304350	3643	F	1158788	5363	B	765018
1924	F	307232	3644	F	1162326	5364	B	763539
1925	F	305310	3645	F	1160468	5365	B	765504
1926	F	307799	3646	F	1163300	5366	B	764000
1927	F	305877	3647	F	1161413	5367	B	765907
1928	F	309173	3648	F	1163763	5368	B	765391
1929	F	307301	3649	F	1161842	5369	B	767328
1930	F	310158	3650	F	1164224	5370	B	767041
1931	F	308306	3651	F	1162283	5371	B	768951
1932	F	311020	3652	F	1164800	5372	B	768271
1933	F	309118	3653	F	1162908	5373	B	770171
1934	F	311031	3654	F	1165312	5374	B	768799
1935	F	309126	3655	F	1163427	5375	B	770686
1936	F	311552	3656	F	1165877	5376	B	769562
1937	F	309658	3657	F	1163960	5377	B	771608
1938	F	312510	3658	F	1166827	5378	B	770752
1939	F	310614	3659	F	1164936	5379	B	772652
1940	F	313134	3660	F	1168099	5380	B	771701
1941	F	311255	3661	F	1166212	5381	B	773620
1942	F	313674	3662	F	1168991	5382	B	773316
1943	F	311717	3663	F	1167093	5383	B	775178
1944	F	314490	3664	F	1169769	5384	B	773690
1945	F	312633	3665	F	1167907	5385	B	775579
1946	F	315306	3666	F	1170349	5386	B	774596
1947	F	313355	3667	F	1168446	5387	B	776522
1948	F	315932	3668	F	1170953	5388	B	776300
1949	F	314033	3669	F	1169031	5389	B	778224
1950	F	318434	3670	F	1171641	5390	B	775346
1951	F	316516	3671	F	1169703	5391	B	777266
1952	F	320876	3672	F	1172172	5392	B	775618
1953	F	318949	3673	F	1170256	5393	B	777518
1954	F	321403	3674	F	1173649	5394	B	777266

1955	F	319547	3675	F	1171759	5395	B	779200
1956	F	322084	3676	F	1174885	5396	B	778224
1957	F	320217	3677	F	1172999	5397	B	780087
1958	F	322911	3678	F	1175559	5398	B	778396
1959	F	321049	3679	F	1173649	5399	B	780301
1960	F	323634	3680	F	1176927	5400	B	779557
1961	F	321726	3681	F	1175025	5401	B	781481
1962	F	325117	3682	F	1178912	5402	B	780503
1963	F	323211	3683	F	1176985	5403	B	782380
1964	F	326213	3684	F	1179826	5404	B	781419
1965	F	324254	3685	F	1177910	5405	B	783311
1966	F	327607	3686	F	1180498	5406	B	781747
1967	F	325695	3687	F	1178666	5407	B	783680
1968	F	328162	3688	F	1181716	5408	B	783004
1969	F	326262	3689	F	1179839	5409	B	784912
1970	F	328630	3690	F	1182069	5410	B	783820
1971	F	326723	3691	F	1180140	5411	B	785752
1972	F	329134	3692	F	1183626	5412	B	785255
1973	F	327178	3693	F	1181716	5413	B	787155
1974	F	330734	3694	F	1184128	5414	B	786655
1975	F	328810	3695	F	1182244	5415	B	788572
1976	F	332123	3696	F	1185004	5416	B	788671
1977	F	330252	3697	F	1183084	5417	B	790554
1978	F	334575	3698	F	1185897	5418	B	789164
1979	F	332660	3699	F	1184029	5419	B	791064
1980	F	335884	3700	F	1187151	5420	B	790001
1981	F	333980	3701	F	1185251	5421	B	791900
1982	F	337129	3702	F	1186262	5422	B	791734
1983	F	335202	3703	F	1184361	5423	B	793679
1984	F	337910	3704	F	1189054	5424	B	792944
1985	F	335955	3705	F	1187160	5425	B	794875
1986	F	338746	3706	F	1190885	5426	B	793809
1987	F	336795	3707	F	1188990	5427	B	795692
1988	F	339217	3708	F	1191507	5428	B	794580
1989	F	337362	3709	F	1189579	5429	B	796450

1990	F	339999	3710	F	1191932	5430	B	795066
1991	F	338083	3711	F	1190008	5431	B	796966
1992	F	343144	3712	F	1192524	5432	B	795956
1993	F	341266	3713	F	1190640	5433	B	797855
1994	F	343699	3714	F	1192759	5434	B	797018
1995	F	341813	3715	F	1190869	5435	B	798918
1996	F	344108	3716	F	1193642	5436	B	798989
1997	F	342204	3717	F	1191742	5437	B	800875
1998	F	344851	3718	F	1193557	5438	B	800069
1999	F	342933	3719	F	1191657	5439	B	801944
2000	F	346148	3720	F	1194015	5440	B	799840
2001	F	344219	3721	F	1192120	5441	B	801701
2002	F	346493	3722	F	1195490	5442	B	801533
2003	F	344590	3723	F	1193560	5443	B	803445
2004	F	346815	3724	F	1196093	5444	B	802717
2005	F	344907	3725	F	1194215	5445	B	804581
2006	F	347836	3726	F	1196474	5446	B	803559
2007	F	345956	3727	F	1194592	5447	B	805419
2008	F	350379	3728	F	1197659	5448	B	804032
2009	F	348432	3729	F	1195724	5449	B	805931
2010	F	350856	3730	F	1198499	5450	B	805383
2011	F	348951	3731	F	1196578	5451	B	807291
2012	F	352008	3732	F	1199912	5452	B	806107
2013	F	350106	3733	F	1197986	5453	B	807988
2014	F	353209	3734	F	1200969	5454	B	806533
2015	F	351305	3735	F	1199133	5455	B	808430
2016	F	354224	3736	F	1202121	5456	B	806954
2017	F	352312	3737	F	1200227	5457	B	808724
2018	F	354781	3738	F	1202957	5458	B	807133
2019	F	352871	3739	F	1201058	5459	B	809033
2020	F	355223	3740	F	1202590	5460	B	808442
2021	F	353261	3741	F	1200694	5461	B	810357
2022	F	355393	3742	F	1203923	5462	B	808972
2023	F	353519	3743	F	1202049	5463	B	810896
2024	F	358901	3744	F	1204631	5464	B	809674

2025	F	357001	3745	F	1202753	5465	B	811557
2026	F	356594	3746	F	1205864	5466	B	810192
2027	F	354692	3747	F	1203964	5467	B	812105
2028	F	359240	3748	F	1206483	5468	B	811472
2029	F	357374	3749	F	1204592	5469	B	813357
2030	F	359721	3750	F	1207629	5470	B	813325
2031	F	357763	3751	F	1205727	5471	B	815179
2032	F	361071	3752	F	1208802	5472	B	813133
2033	F	359240	3753	F	1206909	5473	B	815134
2034	F	363605	3754	F	1209500	5474	B	813808
2035	F	361731	3755	F	1207557	5475	B	815737
2036	F	364142	3756	F	1210483	5476	B	815246
2037	F	362246	3757	F	1208584	5477	B	817168
2038	F	364567	3758	F	1211618	5478	B	815995
2039	F	362708	3759	F	1209745	5479	B	817892
2040	F	365039	3760	F	1212523	5480	B	817264
2041	F	363184	3761	F	1210554	5481	B	819164
2042	F	365445	3762	F	1213827	5482	B	817579
2043	F	363517	3763	F	1211927	5483	B	819491
2044	F	367040	3764	F	1214875	5484	B	818890
2045	F	365144	3765	F	1212992	5485	B	820733
2046	F	368825	3766	F	1215293	5486	B	819332
2047	F	366993	3767	F	1213430	5487	B	821217
2048	F	369698	3768	F	1216043	5488	B	820096
2049	F	367760	3769	F	1214183	5489	B	821951
2050	F	370141	3770	F	1216226	5490	B	820945
2051	F	368239	3771	F	1214374	5491	B	822870
2052	F	372329	3772	F	1216927	5492	B	821151
2053	F	370375	3773	F	1215064	5493	B	823079
2054	F	372779	3774	F	1219490	5494	B	822558
2055	F	370881	3775	F	1217534	5495	B	824449
2056	F	373223	3776	F	1219431	5496	B	823767
2057	F	371342	3777	F	1217534	5497	B	825634
2058	F	373939	3778	F	1220403	5498	B	825876
2059	F	372017	3779	F	1218475	5499	B	827737

2060	F	374849	3780	F	1221383	5500	B	826583
2061	F	372953	3781	F	1219499	5501	B	828435
2062	F	375351	3782	F	1223653	5502	B	827511
2063	F	373487	3783	F	1221767	5503	B	829428
2064	F	376316	3784	F	1224758	5504	B	828829
2065	F	374416	3785	F	1222881	5505	B	830729
2066	F	377737	3786	F	1226308	5506	B	830262
2067	F	375828	3787	F	1224409	5507	B	832158
2068	F	379537	3788	F	1225625	5508	B	831286
2069	F	377660	3789	F	1223654	5509	B	833182
2070	F	380033	3790	F	1227566	5510	B	831946
2071	F	378160	3791	F	1225677	5511	B	833848
2072	F	380789	3792	F	1227858	5512	B	833372
2073	F	378889	3793	F	1225937	5513	B	835267
2074	F	381238	3794	F	1228081	5514	B	834125
2075	F	379279	3795	F	1226189	5515	B	835992
2076	F	382969	3796	B	1019	5516	B	835267
2077	F	381124	3797	B	2954	5517	B	837193
2078	F	383293	3798	B	1843	5518	B	836111
2079	F	381425	3799	B	3739	5519	B	837952
2080	F	385178	3800	B	2694	5520	B	837844
2081	F	383278	3801	B	4545	5521	B	839751
2082	F	386271	3802	B	3694	5522	B	839381
2083	F	384392	3803	B	5513	5523	B	841221
2084	F	386780	3804	B	4290	5524	B	841127
2085	F	384891	3805	B	6238	5525	B	843073
2086	F	389383	3806	B	5924	5526	B	842409
2087	F	387504	3807	B	7846	5527	B	844323
2088	F	389901	3808	B	7687	5528	B	843691
2089	F	388001	3809	B	9583	5529	B	845602
2090	F	390700	3810	B	9189	5530	B	844244
2091	F	388732	3811	B	11095	5531	B	846153
2092	F	391612	3812	B	10261	5532	B	845319
2093	F	389763	3813	B	12119	5533	B	847139
2094	F	392346	3814	B	10982	5534	B	846411

2095	F	390463	3815	B	12839	5535	B	848300
2096	F	392540	3816	B	11463	5536	B	848760
2097	F	390639	3817	B	13355	5537	B	850653
2098	F	393487	3818	B	12950	5538	B	849242
2099	F	391609	3819	B	14850	5539	B	851174
2100	F	393904	3820	B	14425	5540	B	850753
2101	F	392025	3821	B	16332	5541	B	852649
2102	F	394703	3822	B	17477	5542	B	851795
2103	F	392782	3823	B	19400	5543	B	853690
2104	F	395024	3824	B	16296	5544	B	852696
2105	F	393098	3825	B	18161	5545	B	854596
2106	F	395705	3826	B	21128	5546	B	853938
2107	F	393791	3827	B	22976	5547	B	855846
2108	F	397607	3828	B	22265	5548	B	855338
2109	F	395705	3829	B	24185	5549	B	857240
2110	F	398807	3830	B	23701	5550	B	855982
2111	F	396957	3831	B	25599	5551	B	857873
2112	F	399848	3832	B	26350	5552	B	856786
2113	F	397886	3833	B	28258	5553	B	858722
2114	F	400914	3834	B	26350	5554	B	858783
2115	F	399008	3835	B	28258	5555	B	860735
2116	F	401183	3836	B	27241	5556	B	859824
2117	F	399301	3837	B	29113	5557	B	861787
2118	F	401964	3838	B	27977	5558	B	860442
2119	F	400060	3839	B	29896	5559	B	862329
2120	F	403450	3840	B	28804	5560	B	861415
2121	F	401527	3841	B	30700	5561	B	863252
2122	F	404124	3842	B	29727	5562	B	861677
2123	F	402206	3843	B	31642	5563	B	863558
2124	F	405765	3844	B	30253	5564	B	863171
2125	F	403865	3845	B	32158	5565	B	865099
2126	F	407131	3846	B	31775	5566	B	865021
2127	F	405243	3847	B	33657	5567	B	866922
2128	F	407456	3848	B	32511	5568	B	865497
2129	F	405563	3849	B	34422	5569	B	867408

2130	F	408841	3850	B	34214	5570	B	866808
2131	F	406901	3851	B	36114	5571	B	868732
2132	F	410478	3852	B	34765	5572	B	867342
2133	F	408573	3853	B	36664	5573	B	869242
2134	F	410725	3854	B	36289	5574	B	868064
2135	F	408832	3855	B	38186	5575	B	869974
2136	F	412263	3856	B	37759	5576	B	868732
2137	F	410363	3857	B	39682	5577	B	870664
2138	F	414168	3858	B	39585	5578	B	869974
2139	F	412268	3859	B	41496	5579	B	871880
2140	F	415013	3860	B	40942	5580	B	870857
2141	F	413111	3861	B	42840	5581	B	872753
2142	F	415636	3862	B	39640	5582	B	872149
2143	F	413743	3863	B	41543	5583	B	874087
2144	F	417033	3864	B	43329	5584	B	872758
2145	F	415114	3865	B	45196	5585	B	874658
2146	F	417163	3866	B	44025	5586	B	874131
2147	F	415332	3867	B	45979	5587	B	876122
2148	F	418166	3868	B	45048	5588	B	874903
2149	F	416265	3869	B	46970	5589	B	876793
2150	F	420186	3870	B	45582	5590	B	875548
2151	F	418259	3871	B	47472	5591	B	877437
2152	F	420697	3872	B	45979	5592	B	878078
2153	F	418861	3873	B	47901	5593	B	880011
2154	F	421313	3874	B	47216	5594	B	879478
2155	F	419437	3875	B	49128	5595	B	881385
2156	F	422172	3876	B	47791	5596	B	880874
2157	F	420342	3877	B	49689	5597	B	882771
2158	F	423342	3878	B	48196	5598	B	882771
2159	F	421412	3879	B	50126	5599	B	884644
2160	F	424008	3880	B	49180	5600	B	883542
2161	F	422073	3881	B	51105	5601	B	885447
2162	F	424585	3882	B	50231	5602	B	883777
2163	F	422711	3883	B	52149	5603	B	885689
2164	F	426021	3884	B	51697	5604	B	884430

2165	F	424107	3885	B	53619	5605	B	886335
2166	F	427407	3886	B	52917	5606	B	885834
2167	F	425513	3887	B	54735	5607	B	887782
2168	F	427936	3888	B	53619	5608	B	887528
2169	F	426053	3889	B	55476	5609	B	889442
2170	F	428592	3890	B	53910	5610	B	888432
2171	F	426717	3891	B	55816	5611	B	890292
2172	F	430475	3892	B	54416	5612	B	888879
2173	F	428558	3893	B	56326	5613	B	890775
2174	F	431378	3894	B	55107	5614	B	889595
2175	F	429417	3895	B	57009	5615	B	891481
2176	F	431927	3896	B	56693	5616	B	890119
2177	F	430046	3897	B	58586	5617	B	892034
2178	F	432609	3898	B	57489	5618	B	891428
2179	F	430710	3899	B	59394	5619	B	893320
2180	F	433005	3900	B	58749	5620	B	892050
2181	F	431082	3901	B	60649	5621	B	893950
2182	F	433712	3902	B	60086	5622	B	892259
2183	F	431812	3903	B	62002	5623	B	894158
2184	F	436521	3904	B	62375	5624	B	892701
2185	F	434640	3905	B	64275	5625	B	894611
2186	F	436897	3906	B	61715	5626	B	893194
2187	F	435057	3907	B	63633	5627	B	895056
2188	F	439741	3908	B	62699	5628	B	893347
2189	F	437882	3909	B	64601	5629	B	895263
2190	F	438296	3910	B	63981	5630	B	893787
2191	F	436377	3911	B	65858	5631	B	895711
2192	F	440475	3912	B	64268	5632	B	895642
2193	F	438538	3913	B	66227	5633	B	897542
2194	F	440281	3914	B	64423	5634	B	896759
2195	F	438394	3915	B	66309	5635	B	898650
2196	F	440989	3916	B	64834	5636	B	897802
2197	F	439080	3917	B	66756	5637	B	899694
2198	F	442121	3918	B	65705	5638	B	899665
2199	F	440252	3919	B	67611	5639	B	901565

2200	F	442121	3920	B	66228	5640	B	900460
2201	F	440221	3921	B	68163	5641	B	902360
2202	F	442780	3922	B	67538	5642	B	903450
2203	F	440879	3923	B	69404	5643	B	905354
2204	F	443285	3924	B	67961	5644	B	905307
2205	F	441384	3925	B	69841	5645	B	907291
2206	F	444276	3926	B	68796	5646	B	907290
2207	F	442406	3927	B	70662	5647	B	909083
2208	F	444472	3928	B	70984	5648	B	908055
2209	F	442568	3929	B	72885	5649	B	909955
2210	F	444960	3930	B	69392	5650	B	908358
2211	F	443040	3931	B	71314	5651	B	910273
2212	F	445556	3932	B	71365	5652	B	908900
2213	F	443681	3933	B	73287	5653	B	910831
2214	F	447565	3934	B	72253	5654	B	909607
2215	F	445676	3935	B	74167	5655	B	911450
2216	F	448396	3936	B	73916	5656	B	911760
2217	F	446496	3937	B	75760	5657	B	913589
2218	F	450057	3938	B	76398	5658	B	912584
2219	F	448133	3939	B	78328	5659	B	914529
2220	F	450444	3940	B	77734	5660	B	913054
2221	F	448555	3941	B	79610	5661	B	914956
2222	F	450988	3942	B	78592	5662	B	914208
2223	F	449054	3943	B	80517	5663	B	916113
2224	F	452212	3944	B	79577	5664	B	915388
2225	F	450329	3945	B	81476	5665	B	917272
2226	F	453450	3946	B	79968	5666	B	915880
2227	F	451581	3947	B	81861	5667	B	917747
2228	F	454643	3948	B	80203	5668	B	916886
2229	F	452718	3949	B	82108	5669	B	918778
2230	F	456004	3950	B	80665	5670	B	917940
2231	F	454124	3951	B	82565	5671	B	919827
2232	F	456785	3952	B	81257	5672	B	919070
2233	F	454897	3953	B	83184	5673	B	920972
2234	F	457749	3954	B	83370	5674	B	920107

2235	F	455856	3955	B	85203	5675	B	922088
2236	F	458132	3956	B	84202	5676	B	920666
2237	F	456205	3957	B	86080	5677	B	922554
2238	F	459216	3958	B	85032	5678	B	921412
2239	F	457348	3959	B	86902	5679	B	923307
2240	F	460692	3960	B	85520	5680	B	922216
2241	F	458792	3961	B	87367	5681	B	924104
2242	F	460133	3962	B	85648	5682	B	922661
2243	F	458230	3963	B	87548	5683	B	924538
2244	F	461228	3964	B	86155	5684	B	924024
2245	F	459327	3965	B	88052	5685	B	925893
2246	F	462183	3966	B	86806	5686	B	924192
2247	F	460269	3967	B	88768	5687	B	926063
2248	F	463120	3968	B	88389	5688	B	925245
2249	F	461220	3969	B	90207	5689	B	927137
2250	F	464355	3970	B	89174	5690	B	925672
2251	F	462444	3971	B	91107	5691	B	927558
2252	F	464842	3972	B	91319	5692	B	926744
2253	F	463010	3973	B	93151	5693	B	928659
2254	F	465346	3974	B	93306	5694	B	928169
2255	F	463451	3975	B	95184	5695	B	930064
2256	F	466061	3976	B	94311	5696	B	928543
2257	F	464143	3977	B	96210	5697	B	930439
2258	F	466780	3978	B	94761	5698	B	929238
2259	F	464842	3979	B	96578	5699	B	931109
2260	F	467462	3980	B	95640	5700	B	931227
2261	F	465578	3981	B	97452	5701	B	933127
2262	F	469419	3982	B	96835	5702	B	932291
2263	F	467538	3983	B	98743	5703	B	934184
2264	F	471324	3984	B	97685	5704	B	933738
2265	F	469419	3985	B	99639	5705	B	935651
2266	F	470463	3986	B	98655	5706	B	933127
2267	F	468587	3987	B	100585	5707	B	935001
2268	F	471822	3988	B	99680	5708	B	935969
2269	F	469897	3989	B	101592	5709	B	937869

2270	F	472471	3990	B	101592	5710	B	937305
2271	F	470610	3991	B	103448	5711	B	939223
2272	F	473208	3992	B	101950	5712	B	937448
2273	F	471319	3993	B	103878	5713	B	939423
2274	F	475143	3994	B	102534	5714	B	938633
2275	F	473243	3995	B	104467	5715	B	940533
2276	F	477091	3996	B	103031	5716	B	939032
2277	F	475181	3997	B	104947	5717	B	940928
2278	F	477375	3998	B	103754	5718	B	939478
2279	F	475475	3999	B	105653	5719	B	941392
2280	F	478473	4000	B	104281	5720	B	940021
2281	F	476586	4001	B	106192	5721	B	941918
2282	F	479058	4002	B	104786	5722	B	941017
2283	F	477158	4003	B	106618	5723	B	942925
2284	F	479829	4004	B	108635	5724	B	941392
2285	F	477916	4005	B	110512	5725	B	943238
2286	F	481237	4006	B	112299	5726	B	941586
2287	F	479312	4007	B	114196	5727	B	943496
2288	F	481769	4008	B	112839	5728	B	942787
2289	F	479903	4009	B	114713	5729	B	944657
2290	F	482435	4010	B	113960	5730	B	943043
2291	F	480535	4011	B	115829	5731	B	944971
2292	F	483976	4012	B	114352	5732	B	943404
2293	F	482075	4013	B	116272	5733	B	945286
2294	F	484899	4014	B	114932	5734	B	944025
2295	F	483029	4015	B	116831	5735	B	945981
2296	F	485593	4016	B	116002	5736	B	944302
2297	F	483674	4017	B	117886	5737	B	946175
2298	F	486401	4018	B	116781	5738	B	944654
2299	F	484498	4019	B	118702	5739	B	946533
2300	F	486762	4020	B	118284	5740	B	945633
2301	F	484859	4021	B	120181	5741	B	947515
2302	F	487287	4022	B	118749	5742	B	946073
2303	F	485366	4023	B	120691	5743	B	947974
2304	F	487487	4024	B	120124	5744	B	946645

2305	F	485642	4025	B	122009	5745	B	948517
2306	F	488811	4026	B	120691	5746	B	947646
2307	F	486942	4027	B	122601	5747	B	949545
2308	F	488918	4028	B	122655	5748	B	948344
2309	F	487001	4029	B	124563	5749	B	950219
2310	F	489740	4030	B	123173	5750	B	950104
2311	F	487772	4031	B	125141	5751	B	952004
2312	F	490300	4032	B	123579	5752	B	951301
2313	F	488400	4033	B	125526	5753	B	953207
2314	F	490880	4034	B	126570	5754	B	951505
2315	F	488969	4035	B	128539	5755	B	953387
2316	F	491167	4036	B	129398	5756	B	952382
2317	F	489268	4037	B	131325	5757	B	954257
2318	F	492066	4038	B	134942	5758	B	952927
2319	F	490096	4039	B	136814	5759	B	954794
2320	F	494600	4040	B	136628	5760	B	953711
2321	F	492697	4041	B	138531	5761	B	955611
2322	F	495778	4042	B	138117	5762	B	955556
2323	F	493845	4043	B	139995	5763	B	957444
2324	F	496350	4044	B	138531	5764	B	956049
2325	F	494396	4045	B	140363	5765	B	957977
2326	F	497139	4046	B	138525	5766	B	957358
2327	F	495210	4047	B	140361	5767	B	959202
2328	F	497504	4048	B	139778	5768	B	958136
2329	F	495651	4049	B	141692	5769	B	960022
2330	F	498216	4050	B	140577	5770	B	959490
2331	F	496381	4051	B	142487	5771	B	961374
2332	F	498990	4052	B	142067	5772	B	960507
2333	F	497076	4053	B	143981	5773	B	962439
2334	F	499284	4054	B	142919	5774	B	961892
2335	F	497401	4055	B	144787	5775	B	963792
2336	F	499563	4056	B	144478	5776	B	965000
2337	F	497644	4057	B	146417	5777	B	966954
2338	F	500555	4058	B	145520	5778	B	967076
2339	F	498645	4059	B	147378	5779	B	968975

2340	F	503868	4060	B	146972	5780	B	968474
2341	F	502008	4061	B	148872	5781	B	970326
2342	F	504574	4062	B	147545	5782	B	969039
2343	F	502741	4063	B	149452	5783	B	970930
2344	F	506571	4064	B	147756	5784	B	969718
2345	F	504671	4065	B	149677	5785	B	971619
2346	F	507498	4066	B	148484	5786	B	970080
2347	F	505565	4067	B	150382	5787	B	971991
2348	F	507615	4068	B	152436	5788	B	970371
2349	F	505777	4069	B	154325	5789	B	972257
2350	F	510441	4070	B	154353	5790	B	970832
2351	F	508522	4071	B	156228	5791	B	972738
2352	F	513523	4072	B	155395	5792	B	971481
2353	F	511660	4073	B	157286	5793	B	973403
2354	F	516834	4074	B	155740	5794	B	971909
2355	F	514938	4075	B	157613	5795	B	973810
2356	F	515101	4076	B	157002	5796	B	975372
2357	F	513277	4077	B	158902	5797	B	977234
2358	F	517031	4078	B	157861	5798	B	975634
2359	F	515093	4079	B	159764	5799	B	977548
2360	F	517620	4080	B	159219	5800	B	976739
2361	F	515698	4081	B	161121	5801	B	978639
2362	F	518070	4082	B	159569	5802	B	978543
2363	F	516181	4083	B	161484	5803	B	980448
2364	F	521162	4084	B	160221	5804	B	977907
2365	F	519241	4085	B	162109	5805	B	979832
2366	F	523023	4086	B	160670	5806	B	980997
2367	F	521123	4087	B	162572	5807	B	982862
2368	F	523865	4088	B	161075	5808	B	982167
2369	F	522003	4089	B	162983	5809	B	984051
2370	F	524373	4090	B	161789	5810	B	983206
2371	F	522530	4091	B	163728	5811	B	985082
2372	F	526029	4092	B	162380	5812	B	984344
2373	F	524115	4093	B	164291	5813	B	986279
2374	F	526479	4094	B	162671	5814	B	985741

2375	F	524580	4095	B	164573	5815	B	987653
2376	F	526756	4096	B	164340	5816	B	986106
2377	F	524823	4097	B	166222	5817	B	988045
2378	F	528167	4098	B	165693	5818	B	987667
2379	F	526263	4099	B	167632	5819	B	989585
2380	F	529315	4100	B	166627	5820	B	987418
2381	F	527408	4101	B	168472	5821	B	989315
2382	F	530372	4102	B	168668	5822	B	987936
2383	F	528484	4103	B	170565	5823	B	989842
2384	F	531842	4104	B	169244	5824	B	988447
2385	F	529945	4105	B	171102	5825	B	990355
2386	F	534077	4106	B	169734	5826	B	988979
2387	F	532190	4107	B	171575	5827	B	990875
2388	F	536335	4108	B	171259	5828	B	990066
2389	F	534585	4109	B	173158	5829	B	991966
2390	F	536858	4110	B	171701	5830	B	991268
2391	F	534931	4111	B	173585	5831	B	993171
2392	F	537710	4112	B	172018	5832	B	991858
2393	F	535810	4113	B	173925	5833	B	993763
2394	F	538105	4114	B	172759	5834	B	992722
2395	F	536211	4115	B	174706	5835	B	994621
2396	F	538901	4116	B	173718	5836	B	993082
2397	F	536979	4117	B	175602	5837	B	994988
2398	F	539360	4118	B	174902	5838	B	993290
2399	F	537421	4119	B	176765	5839	B	995230
2400	F	541059	4120	B	175869	5840	B	995015
2401	F	539160	4121	B	177781	5841	B	996927
2402	F	542198	4122	B	176181	5842	B	993839
2403	F	540335	4123	B	178083	5843	B	995750
2404	F	542650	4124	B	177158	5844	B	996203
2405	F	540840	4125	B	179120	5845	B	998090
2406	F	543589	4126	B	177599	5846	B	997094
2407	F	541677	4127	B	179539	5847	B	998977
2408	F	546376	4128	B	177928	5848	B	997835
2409	F	544486	4129	B	179888	5849	B	999728

2410	F	546731	4130	B	179693	5850	B	999224
2411	F	544872	4131	B	181621	5851	B	1001101
2412	F	549480	4132	B	180070	5852	B	1000267
2413	F	547547	4133	B	181968	5853	B	1002146
2414	F	550245	4134	B	182017	5854	B	1001594
2415	F	548328	4135	B	183925	5855	B	1003567
2416	F	551224	4136	B	182865	5856	B	1002100
2417	F	549328	4137	B	184809	5857	B	1003941
2418	F	552433	4138	B	184640	5858	B	1003571
2419	F	550520	4139	B	186551	5859	B	1005412
2420	F	554767	4140	B	185253	5860	B	1004381
2421	F	552882	4141	B	187108	5861	B	1006269
2422	F	555444	4142	B	185703	5862	B	1004753
2423	F	553541	4143	B	187661	5863	B	1006691
2424	F	557979	4144	B	186129	5864	B	1005890
2425	F	556089	4145	B	188059	5865	B	1007762
2426	F	557923	4146	B	186395	5866	B	1006199
2427	F	555988	4147	B	188339	5867	B	1008109
2428	F	561193	4148	B	188056	5868	B	1007050
2429	F	559292	4149	B	189840	5869	B	1008929
2430	F	559671	4150	B	191218	5870	B	1007819
2431	F	557777	4151	B	193089	5871	B	1009683
2432	F	561555	4152	B	191880	5872	B	1009446
2433	F	559655	4153	B	193768	5873	B	1011365
2434	F	563727	4154	B	193026	5874	B	1010314
2435	F	561828	4155	B	194899	5875	B	1012109
2436	F	564714	4156	B	193709	5876	B	1015234
2437	F	562803	4157	B	195592	5877	B	1017133
2438	F	566079	4158	B	194284	5878	B	1016571
2439	F	564180	4159	B	196187	5879	B	1018486
2440	F	567470	4160	B	194284	5880	B	1017755
2441	F	565569	4161	B	196187	5881	B	1019661
2442	F	568454	4162	B	196032	5882	B	1016781
2443	F	566609	4163	B	197932	5883	B	1018708
2444	F	569194	4164	B	196298	5884	B	1017022

2445	F	567291	4165	B	198245	5885	B	1018924
2446	F	570873	4166	B	198296	5886	B	1019233
2447	F	568996	4167	B	200200	5887	B	1021143
2448	F	571678	4168	B	199677	5888	B	1019674
2449	F	569809	4169	B	201577	5889	B	1021630
2450	F	571983	4170	B	203050	5890	B	1021020
2451	F	570083	4171	B	204943	5891	B	1022923
2452	F	571837	4172	B	204776	5892	B	1021630
2453	F	569998	4173	B	206682	5893	B	1023525
2454	F	572927	4174	B	205877	5894	B	1024510
2455	F	571022	4175	B	207768	5895	B	1026410
2456	F	574804	4176	B	207568	5896	B	1024936
2457	F	572868	4177	B	209477	5897	B	1026858
2458	F	576267	4178	B	208009	5898	B	1025836
2459	F	574354	4179	B	209935	5899	B	1027677
2460	F	577925	4180	B	208490	5900	B	1027197
2461	F	576082	4181	B	210396	5901	B	1029089
2462	F	578598	4182	B	209832	5902	B	1028022
2463	F	576721	4183	B	211779	5903	B	1029936
2464	F	579758	4184	B	210948	5904	B	1031445
2465	F	577878	4185	B	212834	5905	B	1033319
2466	F	579620	4186	B	211360	5906	B	1031943
2467	F	577731	4187	B	213221	5907	B	1033839
2468	F	579950	4188	B	212036	5908	B	1033277
2469	F	578022	4189	B	213948	5909	B	1035186
2470	F	581080	4190	B	212409	5910	B	1033697
2471	F	579248	4191	B	214308	5911	B	1035554
2472	F	581459	4192	B	214299	5912	B	1034009
2473	F	579555	4193	B	216199	5913	B	1035943
2474	F	582128	4194	B	215173	5914	B	1036282
2475	F	580221	4195	B	217077	5915	B	1038161
2476	F	583209	4196	B	215689	5916	B	1037178
2477	F	581305	4197	B	217544	5917	B	1039088
2478	F	584650	4198	B	216374	5918	B	1037902
2479	F	582828	4199	B	218284	5919	B	1039802

2480	F	585407	4200	B	216932	5920	B	1038167
2481	F	583467	4201	B	218839	5921	B	1040079
2482	F	586579	4202	B	217507	5922	B	1039198
2483	F	584650	4203	B	219410	5923	B	1041036
2484	F	587655	4204	B	218089	5924	B	1040803
2485	F	585772	4205	B	220031	5925	B	1042721
2486	F	587899	4206	B	218491	5926	B	1042560
2487	F	586058	4207	B	220380	5927	B	1044460
2488	F	589079	4208	B	218839	5928	B	1043630
2489	F	587173	4209	B	220716	5929	B	1045526
2490	F	590446	4210	B	219152	5930	B	1044850
2491	F	588616	4211	B	221152	5931	B	1046748
2492	F	592279	4212	B	220125	5932	B	1045609
2493	F	590407	4213	B	221963	5933	B	1047551
2494	F	592585	4214	B	221602	5934	B	1046761
2495	F	590716	4215	B	223507	5935	B	1048677
2496	F	593527	4216	B	222939	5936	B	1047741
2497	F	591593	4217	B	224878	5937	B	1049700
2498	F	594047	4218	B	223791	5938	B	1050218
2499	F	592210	4219	B	225688	5939	B	1052151
2500	F	595658	4220	B	224019	5940	B	1050831
2501	F	593758	4221	B	225909	5941	B	1052744
2502	F	596225	4222	B	224491	5942	B	1051223
2503	F	594387	4223	B	226407	5943	B	1053071
2504	F	596964	4224	B	225279	5944	B	1051974
2505	F	595006	4225	B	227131	5945	B	1053854
2506	F	597536	4226	B	225798	5946	B	1052287
2507	F	595635	4227	B	227692	5947	B	1054238
2508	F	598383	4228	B	227030	5948	B	1053379
2509	F	596448	4229	B	228925	5949	B	1055253
2510	F	599154	4230	B	228032	5950	B	1054458
2511	F	597254	4231	B	229939	5951	B	1056325
2512	F	600368	4232	B	228555	5952	B	1055816
2513	F	598433	4233	B	230455	5953	B	1057680
2514	F	600665	4234	B	228925	5954	B	1056172

2515	F	598769	4235	B	230828	5955	B	1058031
2516	F	602011	4236	B	229587	5956	B	1056825
2517	F	600087	4237	B	231371	5957	B	1058710
2518	F	602418	4238	B	231239	5958	B	1057197
2519	F	600513	4239	B	233111	5959	B	1059089
2520	F	602921	4240	B	231737	5960	B	1058522
2521	F	601009	4241	B	233660	5961	B	1060355
2522	F	604391	4242	B	232306	5962	B	1058919
2523	F	602468	4243	B	234186	5963	B	1060810
2524	F	605571	4244	B	233044	5964	B	1059646
2525	F	603671	4245	B	234873	5965	B	1061521
2526	F	606334	4246	B	234599	5966	B	1060801
2527	F	604452	4247	B	236504	5967	B	1062701
2528	F	607133	4248	B	233738	5968	B	1061774
2529	F	605167	4249	B	235682	5969	B	1063687
2530	F	608673	4250	B	235454	5970	B	1062682
2531	F	606773	4251	B	237347	5971	B	1064555
2532	F	609710	4252	B	235569	5972	B	1064300
2533	F	607794	4253	B	237469	5973	B	1066236
2534	F	610711	4254	B	236954	5974	B	1065489
2535	F	608882	4255	B	238812	5975	B	1067386
2536	F	611524	4256	B	237891	5976	B	1067725
2537	F	609623	4257	B	239761	5977	B	1069601
2538	F	612119	4258	B	238568	5978	B	1068285
2539	F	610213	4259	B	240472	5979	B	1070188
2540	F	613820	4260	B	239227	5980	B	1068930
2541	F	611861	4261	B	241122	5981	B	1070898
2542	F	614604	4262	B	240341	5982	B	1070188
2543	F	612704	4263	B	242266	5983	B	1072078
2544	F	614960	4264	B	241805	5984	B	1071383
2545	F	613056	4265	B	243697	5985	B	1073283
2546	F	616387	4266	B	242570	5986	B	1072658
2547	F	614471	4267	B	244401	5987	B	1074584
2548	F	617574	4268	B	243155	5988	B	1073699
2549	F	615586	4269	B	245067	5989	B	1075652

2550	F	619430	4270	B	243636	5990	B	1076111
2551	F	617510	4271	B	245538	5991	B	1077988
2552	F	618561	4272	B	244754	5992	B	1077010
2553	F	616679	4273	B	246679	5993	B	1078959
2554	F	619799	4274	B	246248	5994	B	1077598
2555	F	617886	4275	B	248169	5995	B	1079390
2556	F	621043	4276	B	248035	5996	B	1078260
2557	F	619133	4277	B	249968	5997	B	1080217
2558	F	622333	4278	B	249397	5998	B	1078959
2559	F	620411	4279	B	251305	5999	B	1080869
2560	F	623110	4280	B	251305	6000	B	1079354
2561	F	621211	4281	B	253161	6001	B	1081215
2562	F	623952	4282	B	252487	6002	B	1080217
2563	F	622052	4283	B	254380	6003	B	1082067
2564	F	624774	4284	B	253274	6004	B	1080742
2565	F	622872	4285	B	255156	6005	B	1082621
2566	F	625263	4286	B	254230	6006	B	1081580
2567	F	623369	4287	B	256130	6007	B	1083489
2568	F	625664	4288	B	255120	6008	B	1083400
2569	F	623773	4289	B	256980	6009	B	1085290
2570	F	626220	4290	B	256331	6010	B	1084927
2571	F	624297	4291	B	258223	6011	B	1086797
2572	F	627684	4292	B	257706	6012	B	1085868
2573	F	625785	4293	B	259578	6013	B	1087768
2574	F	628536	4294	B	258488	6014	B	1086965
2575	F	626655	4295	B	260396	6015	B	1088872
2576	F	629438	4296	B	258089	6016	B	1088185
2577	F	627541	4297	B	260005	6017	B	1090076
2578	F	631496	4298	B	259202	6018	B	1088704
2579	F	629606	4299	B	261035	6019	B	1090504
2580	F	633301	4300	B	261140	6020	B	1089236
2581	F	631397	4301	B	263031	6021	B	1091181
2582	F	637012	4302	B	261834	6022	B	1090076
2583	F	635112	4303	B	263716	6023	B	1091944
2584	F	638002	4304	B	263031	6024	B	1093259

2585	F	636114	4305	B	264890	6025	B	1095056
2586	F	638598	4306	B	263293	6026	B	1093403
2587	F	636682	4307	B	265179	6027	B	1095301
2588	F	638836	4308	B	264599	6028	B	1094437
2589	F	636938	4309	B	266560	6029	B	1096375
2590	F	639333	4310	B	266208	6030	B	1095839
2591	F	637471	4311	B	268109	6031	B	1097798
2592	F	640506	4312	B	266867	6032	B	1096858
2593	F	638598	4313	B	268783	6033	B	1098751
2594	F	640730	4314	B	267558	6034	B	1097305
2595	F	638885	4315	B	269472	6035	B	1099205
2596	F	641468	4316	B	268249	6036	B	1097835
2597	F	639550	4317	B	270042	6037	B	1099724
2598	F	642029	4318	B	269121	6038	B	1098097
2599	F	640162	4319	B	271051	6039	B	1100046
2600	F	642785	4320	B	269709	6040	B	1098615
2601	F	640954	4321	B	271643	6041	B	1100561
2602	F	643129	4322	B	271051	6042	B	1099098
2603	F	641229	4323	B	272920	6043	B	1100975
2604	F	643440	4324	B	271761	6044	B	1099614
2605	F	641522	4325	B	273662	6045	B	1101442
2606	F	645316	4326	B	272570	6046	B	1099747
2607	F	643376	4327	B	274469	6047	B	1101651
2608	F	645552	4328	B	273370	6048	B	1101298
2609	F	643613	4329	B	275313	6049	B	1103227
2610	F	646025	4330	B	273884	6050	B	1102435
2611	F	644186	4331	B	275821	6051	B	1104381
2612	F	646773	4332	B	274219	6052	B	1105179
2613	F	644904	4333	B	276115	6053	B	1107090
2614	F	647678	4334	B	274796	6054	B	1106770
2615	F	645712	4335	B	276716	6055	B	1108631
2616	F	648128	4336	B	275980	6056	B	1107502
2617	F	646249	4337	B	277886	6057	B	1109392
2618	F	650179	4338	B	276241	6058	B	1108337
2619	F	648244	4339	B	278138	6059	B	1110240

2620	F	651010	4340	B	276716	6060	B	1108653
2621	F	649149	4341	B	278625	6061	B	1110570
2622	F	652904	4342	B	277185	6062	B	1113632
2623	F	651003	4343	B	279054	6063	B	1115499
2624	F	653946	4344	B	277489	6064	B	1115225
2625	F	652070	4345	B	279380	6065	B	1117081
2626	F	655735	4346	B	277886	6066	B	1117154
2627	F	653827	4347	B	279722	6067	B	1119051
2628	F	656759	4348	B	278125	6068	B	1118403
2629	F	654894	4349	B	280012	6069	B	1120310
2630	F	658287	4350	B	278841	6070	B	1120257
2631	F	656399	4351	B	280733	6071	B	1122178
2632	F	659973	4352	B	279577	6072	B	1120776
2633	F	658109	4353	B	281466	6073	B	1122682
2634	F	662935	4354	B	280672	6074	B	1121660
2635	F	661035	4355	B	282564	6075	B	1123554
2636	F	664393	4356	B	281767	6076	B	1122120
2637	F	662513	4357	B	283676	6077	B	1123999
2638	F	665972	4358	B	282564	6078	B	1123243
2639	F	664090	4359	B	284462	6079	B	1125024
2640	F	666765	4360	B	284311	6080	B	1123752
2641	F	664879	4361	B	286210	6081	B	1125688
2642	F	667690	4362	B	284740	6082	B	1124484
2643	F	665707	4363	B	286647	6083	B	1126360
2644	F	668261	4364	B	285998	6084	B	1125020
2645	F	666370	4365	B	287975	6085	B	1126928
2646	F	668934	4366	B	286210	6086	B	1125790
2647	F	667029	4367	B	288110	6087	B	1127735
2648	F	670871	4368	B	287201	6088	B	1126747
2649	F	668964	4369	B	289106	6089	B	1128662
2650	F	670629	4370	B	287803	6090	B	1127899
2651	F	668715	4371	B	289737	6091	B	1129808
2652	F	672231	4372	B	288217	6092	B	1128819
2653	F	670334	4373	B	290112	6093	B	1130695
2654	F	672846	4374	B	288417	6094	B	1129798

2655	F	670946	4375	B	290319	6095	B	1131693
2656	F	674040	4376	B	289106	6096	B	1131563
2657	F	672139	4377	B	290961	6097	B	1133490
2658	F	674573	4378	B	289459	6098	B	1132846
2659	F	672674	4379	B	291358	6099	B	1134684
2660	F	675234	4380	B	289914	6100	B	1134070
2661	F	673377	4381	B	291796	6101	B	1136016
2662	F	675834	4382	B	290477	6102	B	1135089
2663	F	673906	4383	B	292423	6103	B	1137037
2664	F	676378	4384	B	290381	6104	B	1135815
2665	F	674477	4385	B	292309	6105	B	1137715
2666	F	676746	4386	B	291463	6106	B	1136186
2667	F	674888	4387	B	293372	6107	B	1138084
2668	F	677769	4388	B	292104	6108	B	1137365
2669	F	675834	4389	B	293999	6109	B	1139255
2670	F	678270	4390	B	293027	6110	B	1140364
2671	F	676378	4391	B	294951	6111	B	1142228
2672	F	679221	4392	B	293507	6112	B	1141611
2673	F	677325	4393	B	295409	6113	B	1143485
2674	F	679874	4394	B	293999	6114	B	1142478
2675	F	677978	4395	B	295838	6115	B	1144291
2676	F	681173	4396	B	294889	6116	B	1145907
2677	F	679288	4397	B	296750	6117	B	1147783
2678	F	680607	4398	B	295312	6118	B	1146953
2679	F	678674	4399	B	297219	6119	B	1148846
2680	F	682210	4400	B	296373	6120	B	1147769
2681	F	680303	4401	B	298305	6121	B	1149703
2682	F	682542	4402	B	298114	6122	B	1148415
2683	F	680607	4403	B	299985	6123	B	1150357
2684	F	683716	4404	B	298656	6124	B	1148758
2685	F	681842	4405	B	300623	6125	B	1150658
2686	F	684312	4406	B	299027	6126	B	1149462
2687	F	682410	4407	B	300899	6127	B	1151258
2688	F	684880	4408	B	299805	6128	B	1149932
2689	F	682916	4409	B	301692	6129	B	1151845

2690	F	685958	4410	B	300722	6130	B	1150814
2691	F	684143	4411	B	302621	6131	B	1152747
2692	F	687264	4412	B	301846	6132	B	1151409
2693	F	685363	4413	B	303706	6133	B	1153285
2694	F	687959	4414	B	302660	6134	B	1152540
2695	F	685958	4415	B	304642	6135	B	1154341
2696	F	688514	4416	B	303066	6136	B	1154863
2697	F	686605	4417	B	304962	6137	B	1156751
2698	F	689372	4418	B	303626	6138	B	1155886
2699	F	687431	4419	B	305479	6139	B	1157813
2700	F	690201	4420	B	304643	6140	B	1156963
2701	F	688318	4421	B	306514	6141	B	1158871
2702	F	691271	4422	B	305479	6142	B	1158093
2703	F	689372	4423	B	307390	6143	B	1159947
2704	F	692436	4424	B	306459	6144	B	1160998
2705	F	690546	4425	B	308393	6145	B	1162864
2706	F	694813	4426	B	307662	6146	B	1162864
2707	F	692930	4427	B	309601	6147	B	1164740
2708	F	695787	4428	B	308298	6148	B	1163244
2709	F	693920	4429	B	310153	6149	B	1165090
2710	F	696363	4430	B	309145	6150	B	1164244
2711	F	694463	4431	B	311044	6151	B	1166175
2712	F	698029	4432	B	310468	6152	B	1164517
2713	F	696133	4433	B	312338	6153	B	1166482
2714	F	699556	4434	B	311437	6154	B	1165167
2715	F	697631	4435	B	313337	6155	B	1167100
2716	F	702303	4436	B	311857	6156	B	1165789
2717	F	700432	4437	B	313860	6157	B	1167710
2718	F	702964	4438	B	311857	6158	B	1166376
2719	F	701079	4439	B	313860	6159	B	1168228
2720	F	704018	4440	B	313015	6160	B	1166872
2721	F	702120	4441	B	314911	6161	B	1168764
2722	F	705018	4442	B	313687	6162	B	1168598
2723	F	703172	4443	B	315549	6163	B	1170498
2724	F	705992	4444	B	313866	6164	B	1169447

2725	F	704105	4445	B	315784	6165	B	1171347
2726	F	706535	4446	B	314911	6166	B	1170043
2727	F	704685	4447	B	316804	6167	B	1171947
2728	F	707455	4448	B	315809	6168	B	1170689
2729	F	705553	4449	B	317701	6169	B	1172616
2730	F	708360	4450	B	316382	6170	B	1171556
2731	F	706385	4451	B	318284	6171	B	1173507
2732	F	708897	4452	B	318881	6172	B	1172305
2733	F	706997	4453	B	320778	6173	B	1174210
2734	F	709589	4454	B	321262	6174	B	1172562
2735	F	707689	4455	B	323214	6175	B	1174508
2736	F	709907	4456	B	321665	6176	B	1174018
2737	F	707963	4457	B	323565	6177	B	1175899
2738	F	711269	4458	B	322571	6178	B	1175429
2739	F	709396	4459	B	324461	6179	B	1177348
2740	F	711864	4460	B	323425	6180	B	1175793
2741	F	709985	4461	B	325316	6181	B	1177675
2742	F	714531	4462	B	324095	6182	B	1177347
2743	F	712594	4463	B	325977	6183	B	1179199
2744	F	715653	4464	B	325135	6184	B	1179316
2745	F	713725	4465	B	327001	6185	B	1181171
2746	F	717511	4466	B	326634	6186	B	1180309
2747	F	715615	4467	B	328557	6187	B	1182212
2748	F	718865	4468	B	328081	6188	B	1181048
2749	F	716993	4469	B	329959	6189	B	1182918
2750	F	720365	4470	B	328719	6190	B	1182162
2751	F	718471	4471	B	330596	6191	B	1184078
2752	F	722155	4472	B	328893	6192	B	1182528
2753	F	720253	4473	B	330825	6193	B	1184437
2754	F	722897	4474	B	329590	6194	B	1184078
2755	F	720989	4475	B	331485	6195	B	1186015
2756	F	723385	4476	B	331127	6196	B	1184698
2757	F	721493	4477	B	333069	6197	B	1186540
2758	F	724029	4478	B	332679	6198	B	1185631
2759	F	722081	4479	B	334592	6199	B	1187530

2760	F	724678	4480	B	334790	6200	B	1186079
2761	F	722749	4481	B	336673	6201	B	1188004
2762	F	726048	4482	B	336311	6202	B	1186704
2763	F	724143	4483	B	338267	6203	B	1188610
2764	F	726897	4484	B	337572	6204	B	1189251
2765	F	724997	4485	B	339431	6205	B	1191165
2766	F	727969	4486	B	338545	6206	B	1187609
2767	F	726086	4487	B	340463	6207	B	1189506
2768	F	728380	4488	B	339058	6208	B	1191165
2769	F	726446	4489	B	341011	6209	B	1193050
2770	F	729281	4490	B	339740	6210	B	1192378
2771	F	727410	4491	B	341628	6211	B	1194291
2772	F	729510	4492	B	340366	6212	B	1192265
2773	F	727579	4493	B	342354	6213	B	1194114
2774	F	729949	4494	B	343265	6214	B	1193058
2775	F	728036	4495	B	345125	6215	B	1194987
2776	F	730367	4496	B	344126	6216	B	1193224
2777	F	728455	4497	B	345957	6217	B	1195115
2778	F	731760	4498	B	344391	6218	B	1194035
2779	F	729866	4499	B	346291	6219	B	1195955
2780	F	732172	4500	B	345324	6220	B	1194384
2781	F	730275	4501	B	347236	6221	B	1196265
2782	F	733018	4502	B	346289	6222	B	1194291
2783	F	731197	4503	B	348198	6223	B	1196205
2784	F	733252	4504	B	347090	6224	B	1195955
2785	F	731354	4505	B	348914	6225	B	1197863
2786	F	733674	4506	B	347292	6226	B	1196570
2787	F	731760	4507	B	349158	6227	B	1198423
2788	F	734054	4508	B	347946	6228	B	1197051
2789	F	732172	4509	B	349851	6229	B	1198951
2790	F	734632	4510	B	350799	6230	B	1198058
2791	F	732736	4511	B	352598	6231	B	1199931
2792	F	735071	4512	B	351313	6232	B	1198960
2793	F	733219	4513	B	353223	6233	B	1200867
2794	F	735381	4514	B	352400	6234	B	1200490

2795	F	733445	4515	B	354357	6235	B	1202395
2796	F	735852	4516	B	353522	6236	B	1201512
2797	F	733957	4517	B	355411	6237	B	1203426
2798	F	736244	4518	B	354690	6238	B	1202606
2799	F	734401	4519	B	356610	6239	B	1204532
2800	F	736982	4520	B	355158	6240	B	1203139
2801	F	735071	4521	B	357057	6241	B	1205063
2802	F	737321	4522	B	355676	6242	B	1203691
2803	F	735397	4523	B	357681	6243	B	1205597
2804	F	737566	4524	B	356995	6244	B	1204382
2805	F	735696	4525	B	358866	6245	B	1206284
2806	F	738491	4526	B	356173	6246	B	1205249
2807	F	736564	4527	B	358074	6247	B	1207170
2808	F	738797	4528	B	359607	6248	B	1206651
2809	F	736935	4529	B	361536	6249	B	1208536
2810	F	739513	4530	B	359550	6250	B	1206976
2811	F	737626	4531	B	361442	6251	B	1208862
2812	F	740420	4532	B	360135	6252	B	1208092
2813	F	738526	4533	B	362033	6253	B	1210002
2814	F	740457	4534	B	361536	6254	B	1209115
2815	F	738599	4535	B	363461	6255	B	1210973
2816	F	741553	4536	B	364013	6256	B	1209979
2817	F	739676	4537	B	365905	6257	B	1211892
2818	F	742518	4538	B	364716	6258	B	1210739
2819	F	740565	4539	B	366707	6259	B	1212639
2820	F	743344	4540	B	365000	6260	B	1211761
2821	F	741509	4541	B	366941	6261	B	1213680
2822	F	743875	4542	B	365513	6262	B	1212985
2823	F	741984	4543	B	367447	6263	B	1214894
2824	F	744240	4544	B	365892	6264	B	1214299
2825	F	742365	4545	B	367873	6265	B	1216189
2826	F	744725	4546	B	366877	6266	B	1215132
2827	F	742858	4547	B	368725	6267	B	1217036
2828	F	746380	4548	B	369265	6268	B	1215714
2829	F	744493	4549	B	371167	6269	B	1217542

2830	F	746957	4550	B	370088	6270	B	1216541
2831	F	745071	4551	B	371988	6271	B	1218462
2832	F	747868	4552	B	370669	6272	B	1216828
2833	F	746023	4553	B	372611	6273	B	1218677
2834	F	748351	4554	B	372871	6274	B	1217166
2835	F	746451	4555	B	374773	6275	B	1218973
2836	F	749395	4556	B	373315	6276	B	1219876
2837	F	747505	4557	B	375227	6277	B	1221743
2838	F	749745	4558	B	373665	6278	B	1220892
2839	F	747857	4559	B	375592	6279	B	1222895
2840	F	750165	4560	B	374428	6280	B	1220288
2841	F	748278	4561	B	376335	6281	B	1222189
2842	F	751013	4562	B	375355	6282	B	1221657
2843	F	749169	4563	B	377248	6283	B	1223517
2844	F	752798	4564	B	375913	6284	B	1223930
2845	F	750889	4565	B	377796	6285	B	1225828
2846	F	754878	4566	B	376483	6286	B	1225211
2847	F	752967	4567	B	378318	6287	B	1227132
2848	F	755856	4568	B	377873	6288	B	1226090
2849	F	754001	4569	B	379798	6289	B	1227979
2850	F	756262	4570	B	380040	6290	B	1227132
2851	F	754372	4571	B	381898	6291	B	1229039
2852	F	760075	4572	B	380699	6292	B	1228061
2853	F	758175	4573	B	382561	6293	B	1229948
2854	F	761069	4574	B	381249	6294	B	1228293
2855	F	759172	4575	B	383174	6295	B	267
2856	F	761549	4576	B	381689	6296	B	1228524
2857	F	759660	4577	B	383629	6297	B	444
2858	F	761988	4578	B	383282	6298	B	267
2859	F	760141	4579	B	385161	6299	B	2068
2860	F	762611	4580	B	383789	6300	F	25997
2861	F	760747	4581	B	385647	6301	F	24032
2862	F	763097	4582	B	385560	6302	F	27128
2863	F	761136	4583	B	387427	6303	F	25189
2864	F	763622	4584	B	386760	6304	F	66744

2865	F	761742	4585	B	388588	6305	F	64845
2866	F	765438	4586	B	387508	6306	F	70130
2867	F	763525	4587	B	389369	6307	F	68200
2868	F	766664	4588	B	388984	6308	F	132477
2869	F	764747	4589	B	390900	6309	F	130559
2870	F	768045	4590	B	390387	6310	F	177854
2871	F	766196	4591	B	392260	6311	F	175906
2872	F	768329	4592	B	391202	6312	F	208127
2873	F	766429	4593	B	393055	6313	F	206180
2874	F	769107	4594	B	392044	6314	F	208688
2875	F	767244	4595	B	393959	6315	F	206807
2876	F	770507	4596	B	392615	6316	F	208732
2877	F	768633	4597	B	394499	6317	F	206877
2878	F	771618	4598	B	393218	6318	F	210051
2879	F	769725	4599	B	395123	6319	F	208141
2880	F	772865	4600	B	393909	6320	F	298801
2881	F	770975	4601	B	395807	6321	F	296907
2882	F	772865	4602	B	394566	6322	F	351495
2883	F	770970	4603	B	396498	6323	F	349572
2884	F	774810	4604	B	395027	6324	F	419727
2885	F	772927	4605	B	396931	6325	F	417822
2886	F	774131	4606	B	395531	6326	F	553133
2887	F	772232	4607	B	397467	6327	F	551247
2888	F	774604	4608	B	396227	6328	F	556301
2889	F	772782	4609	B	398132	6329	F	554410
2890	F	775851	4610	B	398070	6330	F	593567
2891	F	773934	4611	B	399935	6331	F	591675
2892	F	777314	4612	B	399189	6332	F	594641
2893	F	775412	4613	B	400970	6333	F	592748
2894	F	777677	4614	B	400351	6334	F	661934
2895	F	775781	4615	B	402208	6335	F	660041
2896	F	778400	4616	B	401465	6336	F	706309
2897	F	776472	4617	B	403507	6337	F	704409
2898	F	779281	4618	B	401705	6338	F	803092
2899	F	777333	4619	B	403666	6339	F	801192

2900	F	780063	4620	B	402461	6340	F	849060
2901	F	778150	4621	B	404410	6341	F	847142
2902	F	780885	4622	B	403507	6342	F	913050
2903	F	778994	4623	B	405356	6343	F	911152
2904	F	781333	4624	B	404421	6344	F	926614
2905	F	779431	4625	B	406295	6345	F	924714
2906	F	782524	4626	B	406160	6346	F	930121
2907	F	780674	4627	B	408052	6347	F	928238
2908	F	783349	4628	B	407645	6348	F	986297
2909	F	781433	4629	B	409450	6349	F	984362
2910	F	785138	4630	B	407922	6350	F	996001
2911	F	783238	4631	B	409744	6351	F	994109
2912	F	786197	4632	B	409039	6352	F	999731
2913	F	784328	4633	B	410960	6353	F	997877
2914	F	788274	4634	B	410673	6354	F	1009782
2915	F	786387	4635	B	412559	6355	F	1007891
2916	F	788679	4636	B	411193	6356	F	1010540
2917	F	786778	4637	B	413064	6357	F	1008671
2918	F	790090	4638	B	412049	6358	F	1012465
2919	F	788213	4639	B	413946	6359	F	1010540
2920	F	791608	4640	B	414525	6360	F	1028431
2921	F	789711	4641	B	416425	6361	F	1026524
2922	F	792499	4642	B	415622	6362	F	1086215
2923	F	790605	4643	B	417559	6363	F	1084362
2924	F	793324	4644	B	416072	6364	F	1118417
2925	F	791440	4645	B	417968	6365	F	1116527
2926	F	794068	4646	B	417351	6366	F	1169595
2927	F	792185	4647	B	419259	6367	F	1167713
2928	F	794998	4648	B	417789	6368	F	1180592
2929	F	793098	4649	B	419748	6369	F	1178709
2930	F	795457	4650	B	418569	6370	F	1182406
2931	F	793582	4651	B	420453	6371	F	1180498
2932	F	796831	4652	B	420345	6372	F	1194573
2933	F	794931	4653	B	422177	6373	F	1192667
2934	F	798455	4654	B	421003	6374	F	1195654

2935	F	796551	4655	B	422873	6375	F	1193753
2936	F	799056	4656	B	421819	6376	B	26870
2937	F	797147	4657	B	423675	6377	B	28721
2938	F	799558	4658	B	422291	6378	B	27835
2939	F	797649	4659	B	424158	6379	B	29730
2940	F	801106	4660	B	423186	6380	B	67456
2941	F	799204	4661	B	425075	6381	B	69351
2942	F	802227	4662	B	424544	6382	B	70820
2943	F	800325	4663	B	426443	6383	B	72708
2944	F	803050	4664	B	424859	6384	B	133173
2945	F	801153	4665	B	426714	6385	B	135068
2946	F	803599	4666	B	426302	6386	B	178637
2947	F	801682	4667	B	428193	6387	B	180518
2948	F	804925	4668	B	427640	6388	B	208864
2949	F	803016	4669	B	429523	6389	B	210727
2950	F	805633	4670	B	428212	6390	B	209376
2951	F	803672	4671	B	430111	6391	B	211305
2952	F	806109	4672	B	428709	6392	B	209483
2953	F	804192	4673	B	430627	6393	B	211383
2954	F	806386	4674	B	430926	6394	B	210875
2955	F	804453	4675	B	432851	6395	B	212766
2956	F	806668	4676	B	431681	6396	B	299694
2957	F	804746	4677	B	433569	6397	B	301582
2958	F	807924	4678	B	432324	6398	B	352312
2959	F	806022	4679	B	434223	6399	B	354200
2960	F	808445	4680	B	433015	6400	B	420390
2961	F	806525	4681	B	434902	6401	B	422291
2962	F	809212	4682	B	433504	6402	B	553822
2963	F	807283	4683	B	435426	6403	B	555736
2964	F	809982	4684	B	434196	6404	B	557050
2965	F	808079	4685	B	436042	6405	B	558930
2966	F	811554	4686	B	436913	6406	B	594583
2967	F	809659	4687	B	438807	6407	B	596527
2968	F	812268	4688	B	437475	6408	B	595405
2969	F	810340	4689	B	439423	6409	B	597289

2970	F	812712	4690	B	438591	6410	B	662614
2971	F	810799	4691	B	440490	6411	B	664530
2972	F	813355	4692	B	440583	6412	B	707138
2973	F	811466	4693	B	442491	6413	B	709063
2974	F	815198	4694	B	440583	6414	B	803951
2975	F	813243	4695	B	442441	6415	B	805790
2976	F	815798	4696	B	441274	6416	B	849771
2977	F	813917	4697	B	443135	6417	B	851730
2978	F	816879	4698	B	441459	6418	B	913917
2979	F	814940	4699	B	443353	6419	B	915796
2980	F	817571	4700	B	442412	6420	B	927331
2981	F	815676	4701	B	444339	6421	B	929238
2982	F	818388	4702	B	443184	6422	B	930857
2983	F	816489	4703	B	445100	6423	B	932735
2984	F	818884	4704	B	443131	6424	B	986987
2985	F	816921	4705	B	445100	6425	B	988912
2986	F	819597	4706	B	443800	6426	B	996771
2987	F	817680	4707	B	445789	6427	B	998623
2988	F	820485	4708	B	444771	6428	B	1000593
2989	F	818555	4709	B	446620	6429	B	1002496
2990	F	820764	4710	B	445100	6430	B	1010541
2991	F	818878	4711	B	446962	6431	B	1012452
2992	F	821982	4712	B	445229	6432	B	1011365
2993	F	820080	4713	B	447187	6433	B	1013249
2994	F	823403	4714	B	445974	6434	B	1013146
2995	F	821559	4715	B	447872	6435	B	1015044
2996	F	825235	4716	B	448028	6436	B	1029168
2997	F	823320	4717	B	449927	6437	B	1031036
2998	F	826405	4718	B	448958	6438	B	1087041
2999	F	824501	4719	B	450858	6439	B	1088885
3000	F	826945	4720	B	449850	6440	B	1119102
3001	F	825046	4721	B	451753	6441	B	1121033
3002	F	828489	4722	B	451103	6442	B	1170355
3003	F	826588	4723	B	453045	6443	B	1172218
3004	F	829813	4724	B	451482	6444	B	1181427

3005	F	827917	4725	B	453330	6445	B	1183338
3006	F	830824	4726	B	452676	6446	B	1183263
3007	F	828906	4727	B	454575	6447	B	1185158
3008	F	831936	4728	B	453884	6448	B	1195296
3009	F	830099	4729	B	455783	6449	B	1197175
3010	F	833126	4730	B	455068	6450	B	1196406
3011	F	831274	4731	B	456963	6451	B	1198306

TABLE 6

<i>clone Name</i>	<i>SEQ ID NO (B)</i>	<i>SEQ ID NO (F)</i>	<i>Chromosomal region</i>
790313H3#	6452	6648	A
790331B1#	6453	6649	A
790233A9#	6454	6650	A
790031G7#	6455	6651	A
890021E4#	6456	6652	A
790021E11#	6457	6653	A
790332G10#	6458	6654	A
790271B6#	6459	6655	A
790253H6#	6460	6656	A
790214E8#	6461	6657	A
790352D2#	6462	6658	A
790373F2#	6463	6659	A
790424A7#	6464	6660	A
790282F3#	6465	6661	A
790272F5#	6466	6662	A
790424F6#	6467	6663	A
890033H11#	6468	6664	A
790264H10#	6469	6665	A
790293A5#	6470	6666	A
790391E8#	6471	6667	A
890022B8#	6472	6668	A
790332B9#	6473	6669	A
790251B9#	6474	6670	A
790344E8#	6475	6671	B
790323F3#	6476	6672	B
790231G2#	6477	6673	B
790341C5#	6478	6674	B
790332H9#	6479	6675	B
890013A8#	6480	6676	B
790394F2#	6481	6677	B
790222G5#	6482	6678	B
790402A10#	6483	6679	B
790283F6#	6484	6680	B

790041H11#	6485	6681	B
790381C7#	6486	6682	B
790213E1#	6487	6683	B
790211C4#	6488	6684	B
790251B5#	6489	6685	B
790043H9#	6490	6686	B
790303F7#	6491	6687	B
790251G5#	6492	6688	B
790044H7#	6493	6689	B
790022E4#	6494	6690	B
790252A8#	6495	6691	B
790313E9#	6496	6692	B
790264G2#	6497	6693	B
790372A4#	6498	6694	B
790411C2#	6499	6695	B
790322B7#	6500	6696	B
790254F7#	6501	6697	B
790323B12#	6502	6698	B
790263E5#	6503	6699	B
790223C8#	6504	6700	B
790231H2#	6505	6701	B
790324E12#	6506	6702	B
790271D7#	6507	6703	B
790222E8#	6508	6704	B
790083G7#	6509	6705	B
790241D3#	6510	6706	B
790303C8#	6511	6707	B
790283F10#	6512	6708	B
790241B7#	6513	6709	B
790373F10#	6514	6710	B
790362F9#	6515	6711	B
790263H8#	6516	6712	B
790393D10#	6517	6713	B
790313D12#	6518	6714	B
890024C6#	6519	6715	B

890024B10#	6520	6716	B
790212E2#	6521	6717	B
790362E10#	6522	6718	B
790344G11#	6523	6719	B
890011D2#	6524	6720	B
790341B11#	6525	6721	B
790064E10#	6526	6722	B
790212E1#	6527	6723	B
790213G5#	6528	6724	B
790331F2#	6529	6725	B
890024B9#	6530	6726	B
790421F5#	6531	6727	B
890014D11#	6532	6728	B
790373F3#	6533	6729	B
790293D4#	6534	6730	B
790211A3#	6535	6731	B
790211H8#	6536	6732	B
790264E7#	6537	6733	B
790292B11#	6538	6734	B
790312A2#	6539	6735	B
890012D5#	6540	6736	B
790012D12#	6541	6737	B
790291E10#	6542	6738	B
790241C9#	6543	6739	B
790343F1#	6544	6740	B
790241D7#	6545	6741	B
790031H7#	6546	6742	B
790081C4#	6547	6743	B
790013B7#	6548	6744	B
790213F3#	6549	6745	B
790292F9#	6550	6746	B
790423F4#	6551	6747	B
790331F3#	6552	6748	B
790222B10#	6553	6749	B
790261G12#	6554	6750	B

790423G10#	6555	6751	B
790392A9#	6556	6752	B
790331B5#	6557	6753	B
790323H3#	6558	6754	B
890014H8#	6559	6755	B
790231B6#	6560	6756	B
790252F7#	6561	6757	B
790392C10#	6562	6758	B
790021D4#	6563	6759	B
790052D10#	6564	6760	B
790261E3#	6565	6761	B
890023E10#	6566	6762	B
790244B7#	6567	6763	B
790383E1#	6568	6764	B
790401B11#	6569	6765	B
790411B5#	6570	6766	B
790423A11#	6571	6767	B
790031A4#	6572	6768	B
790241G3#	6573	6769	B
790044F7#	6574	6770	B
790252B10#	6575	6771	B
790293F9#	6576	6772	B
790282H3#	6577	6773	B
790381C10#	6578	6774	B
790024H5#	6579	6775	B
790354H7#	6580	6776	B
790411F9#	6581	6777	B
790324G10#	6582	6778	B
790014A5#	6583	6779	B
790381F3#	6584	6780	B
790424D3#	6585	6781	B
790394A10#	6586	6782	B
790423C10#	6587	6783	B
790214D6#	6588	6784	B
790214C4#	6589	6785	B

790014F11#	6590	6786	B
790352F10#	6591	6787	B
790381H6#	6592	6788	B
790282G5#	6593	6789	B
790263C8#	6594	6790	B
890022B4#	6595	6791	B
790283C6#	6596	6792	B
790293B2#	6597	6793	B
790073A3#	6598	6794	B
790313E10#	6599	6795	B
790361D3#	6600	6796	B
790014A11#	6601	6797	B
790254G2#	6602	6798	B
790381C6#	6603	6799	B
790424E3#	6604	6800	B
790421G8#	6605	6801	B
790013C3#	6606	6802	B
790263E8#	6607	6803	B
790373C1#	6608	6804	B
790041C1#	6609	6805	B
790344A7#	6610	6806	B
790271D6#	6611	6807	B
790342H2#	6612	6808	B
890021A6#	6613	6809	B
790381E7#	6614	6810	C
790013G10#	6615	6811	C
790254A4#	6616	6812	C
790213D8#	6617	6813	C
790052A4#	6618	6814	C
790213D3#	6619	6815	C
790394D2#	6620	6816	C
790214D2#	6621	6817	C
790014A4#	6622	6818	C
790324H4#	6623	6819	C
790082B4#	6624	6820	C

790324A6#	6625	6821	C
790424A12#	6626	6822	C
790044G8#	6627	6823	C
790323C6#	6628	6824	C
790312G4#	6629	6825	C
790053C11#	6630	6826	C
890022B7#	6631	6827	C
790392A2#	6632	6828	C
890023D8#	6633	6829	C
790301F1#	6634	6830	C
790343A11#	6635	6831	C
790421A2#	6636	6832	C
790271G2#	6637	6833	C
790302G12#	6638	6834	C
790341E5#	6639	6835	C
790283B6#	6640	6836	C
790222A4#	6641	6837	C
790241B8#	6642	6838	C
790014C2#	6643	6839	C
790402C1#	6644	6840	C
790264E9#	6645	6841	C
790242G4#	6646	6842	C
790422F3#	6647	6843	C

TABLE 7

<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>
6452	B	29372	6583	B	547718	6714	F	519646
6453	B	30198	6584	B	547184	6715	F	520201
6454	B	31007	6585	B	547684	6716	F	520563
6455	B	31126	6586	B	547342	6717	F	521015
6456	B	32735	6587	B	548946	6718	F	521162
6457	B	32264	6588	B	549071	6719	F	521543
6458	B	32898	6589	B	550054	6720	F	521739
6459	B	33582	6590	B	549989	6721	F	522328
6460	B	33519	6591	B	550426	6722	F	522567
6461	B	34836	6592	B	550055	6723	F	522915
6462	B	35795	6593	B	550132	6724	F	523300
6463	B	35548	6594	B	550132	6725	F	523791
6464	B	35825	6595	B	551400	6726	F	523959
6465	B	37239	6596	B	551572	6727	F	524369
6466	B	36761	6597	B	551468	6728	F	524801
6467	B	37045	6598	B	550849	6729	F	525085
6468	B	36761	6599	B	552137	6730	F	525241
6469	B	37958	6600	B	552325	6731	F	525738
6470	B	38636	6601	B	552583	6732	F	526263
6471	B	39813	6602	B	553033	6733	F	526628
6472	B	41140	6603	B	553629	6734	F	526779
6473	B	40575	6604	B	553960	6735	F	527004
6474	B	40526	6605	B	553914	6736	F	527230
6475	B	501495	6606	B	554354	6737	F	527381
6476	B	502410	6607	B	555783	6738	F	527545
6477	B	502586	6608	B	555687	6739	F	527691
6478	B	503233	6609	B	556441	6740	F	527932
6479	B	503749	6610	B	557054	6741	F	527995
6480	B	504488	6611	B	556627	6742	F	528167
6481	B	504206	6612	B	557292	6743	F	528610
6482	B	504310	6613	B	557050	6744	F	529063
6483	B	505455	6614	B	815995	6745	F	529710
6484	B	505877	6615	B	817104	6746	F	531140

6485	B	506655	6616	B	817104	6747	F	531488
6486	B	506513	6617	B	816920	6748	F	531842
6487	B	507532	6618	B	820464	6749	F	532064
6488	B	507742	6619	B	821017	6750	F	532350
6489	B	508050	6620	B	821379	6751	F	532794
6490	B	507771	6621	B	821504	6752	F	533117
6491	B	509120	6622	B	822723	6753	F	533536
6492	B	509646	6623	B	823298	6754	F	533868
6493	B	510137	6624	B	823380	6755	F	534200
6494	B	510953	6625	B	824414	6756	F	534844
6495	B	511165	6626	B	824204	6757	F	535213
6496	B	511526	6627	B	825288	6758	F	535678
6497	B	511993	6628	B	825346	6759	F	535970
6498	B	513012	6629	B	825403	6760	F	536504
6499	B	512983	6630	B	826237	6761	F	537013
6500	B	512781	6631	B	824995	6762	F	537710
6501	B	514155	6632	B	826838	6763	F	538047
6502	B	515036	6633	B	828146	6764	F	538353
6503	B	515287	6634	B	827878	6765	F	538718
6504	B	516292	6635	B	827571	6766	F	539188
6505	B	516234	6636	B	828472	6767	F	539471
6506	B	516337	6637	B	828484	6768	F	539910
6507	B	517347	6638	B	828691	6769	F	540774
6508	B	517005	6639	B	829507	6770	F	540962
6509	B	516888	6640	B	829169	6771	F	541721
6510	B	516234	6641	B	828763	6772	F	542198
6511	B	517560	6642	B	829769	6773	F	542644
6512	B	517337	6643	B	831582	6774	F	543180
6513	B	518756	6644	B	830481	6775	F	543877
6514	B	518943	6645	B	831468	6776	F	544601
6515	B	519833	6646	B	831670	6777	F	544866
6516	B	520123	6647	B	832293	6778	F	545442
6517	B	520574	6648	F	28484	6779	F	545948
6518	B	520888	6649	F	29043	6780	F	546209
6519	B	522154	6650	F	29656	6781	F	546585

6520	B	523041	6651	F	30157	6782	F	546960
6521	B	522052	6652	F	30712	6783	F	547114
6522	B	522217	6653	F	31175	6784	F	547726
6523	B	523035	6654	F	31658	6785	F	548045
6524	B	524995	6655	F	31902	6786	F	548480
6525	B	523567	6656	F	32638	6787	F	548561
6526	B	523477	6657	F	33203	6788	F	548775
6527	B	523967	6658	F	33804	6789	F	549037
6528	B	525211	6659	F	34164	6790	F	549153
6529	B	525215	6660	F	34426	6791	F	549597
6530	B	526133	6661	F	35131	6792	F	550049
6531	B	525674	6662	F	35675	6793	F	550520
6532	B	526561	6663	F	36097	6794	F	550890
6533	B	526697	6664	F	36641	6795	F	550997
6534	B	526715	6665	F	36835	6796	F	551040
6535	B	526844	6666	F	37236	6797	F	551247
6536	B	527261	6667	F	38287	6798	F	551854
6537	B	527503	6668	F	38711	6799	F	552333
6538	B	528775	6669	F	39117	6800	F	552603
6539	B	528249	6670	F	39798	6801	F	552823
6540	B	530307	6671	F	500539	6802	F	553207
6541	B	527772	6672	F	501016	6803	F	553898
6542	B	529406	6673	F	501319	6804	F	554298
6543	B	527752	6674	F	501632	6805	F	554767
6544	B	529829	6675	F	502155	6806	F	555323
6545	B	529907	6676	F	502623	6807	F	555595
6546	B	529574	6677	F	503025	6808	F	555965
6547	B	529635	6678	F	503681	6809	F	556248
6548	B	530391	6679	F	504389	6810	F	815116
6549	B	531516	6680	F	504744	6811	F	815376
6550	B	532154	6681	F	505468	6812	F	815849
6551	B	532606	6682	F	505652	6813	F	816098
6552	B	533407	6683	F	505822	6814	F	818726
6553	B	533664	6684	F	505833	6815	F	819337
6554	B	533916	6685	F	506933	6816	F	820080

6555	B	534707
6556	B	533482
6557	B	534614
6558	B	534935
6559	B	536823
6560	B	535986
6561	B	536143
6562	B	537505
6563	B	537618
6564	B	538165
6565	B	538702
6566	B	540278
6567	B	539156
6568	B	539619
6569	B	540115
6570	B	540724
6571	B	541484
6572	B	540968
6573	B	542062
6574	B	541898
6575	B	543100
6576	B	543846
6577	B	543820
6578	B	544382
6579	B	545158
6580	B	545678
6581	B	545905
6582	B	546683

6686	F	507220
6687	F	507559
6688	F	508216
6689	F	508619
6690	F	509329
6691	F	509783
6692	F	510383
6693	F	510729
6694	F	511188
6695	F	511773
6696	F	511869
6697	F	512946
6698	F	513202
6699	F	513821
6700	F	514322
6701	F	514811
6702	F	515101
6703	F	515611
6704	F	515911
6705	F	516123
6706	F	516169
6707	F	516215
6708	F	516305
6709	F	517240
6710	F	517993
6711	F	518174
6712	F	518756
6713	F	519133

6817	F	820750
6818	F	821170
6819	F	821815
6820	F	822490
6821	F	822789
6822	F	823244
6823	F	823762
6824	F	823964
6825	F	824245
6826	F	824609
6827	F	824948
6828	F	825490
6829	F	826064
6830	F	826405
6831	F	826480
6832	F	827089
6833	F	827418
6834	F	827496
6835	F	827730
6836	F	828180
6837	F	828348
6838	F	828729
6839	F	830099
6840	F	830281
6841	F	830491
6842	F	830550
6843	F	830576

Publications Cited in the Specification

- Adames et al., 1985, Nature, 318 : 533-538.
- Aldous, M.B. et al., 1992, J. Infect. Dis., 166 : 646-649.
- 5 Alexander et al., 1987, Mol. Cell. Biol., 7 : 1436-1444.
- Allan, G. M. et al., 1995, Vet. Microbiol., 44 : 49-64.
- Altschul, S.F. et al., 1990, J. Mol. Biol., 215 : 403-410.
- Altschul et al., 1993, Nature Genetics, 3 : 266-272.
- Altschul et al., 1997, Nucl. Acids Res., 25 : 3389-3402.
- 10 Ansubel et al., 1989, Current Protocols in Molecular Biology,
- Arlinghaus, H.F. et al., 1997, Anal. Biochem., 69, 18, 3747-53.
- Bai, M. Et al., 1993, J. Virol., 67 : 5198-5205.
- Barany, F., 1911, PNAS USA, 88 : 189-193.
- Beattie, K. et al., 1993, Clin. Chem., 39(4) : 719-721.
- 15 Bernoist and Chambon, 1981, Nature, 290 : 304-310.
- Borman, S., 1996, Chem. Eng. News, 74(50) : 42-43.
- Braun, J. et al., 1994 Ann., Rheum Dis 53 : 100-105.
- Brinster et al., 1982, Nature, 296 : 39-42.
- Buckholz, R.G., 1993, Yeast systems for the expression of heterologous gene products. Curr. Op.
- 20 Biotechnology 4 : 538-542.
- Burg, J.L. et al., 1996, Mol. and Cell. Probes, 10 : 257-271.
- Campbell, L.A. et al., 1992 J. Clin. Microbiol. 30 : 434-439.
- Casas-Ciria J. et al., 1996
- Chatelier, R.C. et al., 1995, Anal. Biochem., 229, 1, 112-118.
- 25 Chee, M. et al., 1996, Science, 274 : 610-613.
- Chu, B.C.F. et al., 1986, NAR, 14 : 5591-5603.
- Chu, P.W.G. et al., 1993, Virus Research, 27 : 161-171.
- Clark, E.G., 1997, American Association of Swine Practitioners, 499-501.
- Cole et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc.,
- 30 pp. 77-96.
- Cote et al., 1983, PNAS USA, 80 : 2026-2030.
- Cserzo, M., Wallin, E., Simon, I. von Heijne G and Elofsson, A., 1997, Prot.
- Eng., 10 : 673-676.
- DeBoer et al., 1980, Scientific American, 242 : 74-94.
- 35 DeBoer et al., 1983, PNAS USA, 80 : 21-25.
- Derisi, J. et al., 1996, Nature Genet, 14 : 457-460.
- Distance Relationships: Atlas of Protein Sequence and Structure, Washington :

- National Biomedical Research Foundation.
- Duck, P. et al., 1990, *Biotechniques*, 9 : 142-147.
- Dulac, G.C. et al., 1989, *Can. J. Vet. Res.*, 53 : 431-433.
- Edwards, C.P., and Aruffo, A., 1993, Current applications of COS cell based transient
5 expression systems. *Curr. Op. Biotechnology* 4 : 558-563.
- Edwards, S. et al., 1994, *Vet. Rec.*, 134 : 680-681.
- Erllich, H.A., 1989, In *PCR Technology. Principles and Applications for DNA
Amplification*. New York : Stockton Press.
- Falsey, et al., *J. Infect. Dis.* 168 :493-496.
- 10 Fanger and Drakeman, 1995, *Drug News and Perspectives*, 8 : 133-137.
- Felgner, et al., 1987, *Proc. Natl. Acad. Sci.*, 84 : 7413.
- Fodor, S.P.A. et al., 1991, *Science*, 251 : 767-771.
- Fontes, E.P.B. et al., 1994, *J. Biol. Chem.*, Vol. 269, N° 11 : 8459-8465.
- Fox, G. Et al., 1989, *J. Gen. Virol.*, 70 : 625-637.
- 15 Fraley et al., 1980, *J. Biol. Chem.*, 255 : 10431.
- Gardner et al., 1981, *Nucl. Acids Res.* 9 : 2871
- Gaydos, C.A. et al., 1994 *J. Clin. Microbiol.* 32 : 903-905.
- Grayston, J.T. et al., 1986 *N. Engl. J. Med.*, 315 : 161-168.
- Grayston, J.T. et al., 1996 *Rev., Med Interne* 17, 45S-47S.
- 20 Gonnet et al., *Science*, 256 : 1443-1445.
- Green Publishing Associates and Wiley Interscience, N.Y.
- Pearson and Lipman, 1988, *PNAS USA*, 85(8) : 2444-2448.
- Grosschedl et al., 1984, *Cell*, 38 : 647-658.
- Guateli, J.C. et al., 1990, *PNAS. USA*, 87 : 1874-1878.
- 25 Hackland, A.F. et al., 1994, *Arch. Virol.*, 139 : 1-22.
- Hahn, D.L. Et al., 1991 *JAMA*. 266
- Haidl, et al., 1992 *N. Engl. J. Med.* 326 :576-577.
- Haidl, et al., *Chlamydial infections* 1994
- Hammer et al., 1987, *Science*, 235 : 53-58.
- 30 Hanahan, 1985, *Nature*, 315 : 115-122.
- Hanson, S.F. et al., 1995, *Virology*, 211 : 1-9.
- Harding, J.C., 1997, *American Association of Swine Practitioners*, 503.
- Harding, R.M. et al., 1993, *Journal of General Virology*, 74 : 323-328.
- Hashiguchi, K. et al., 1992 *J. Laryngol. Otol.* 106 : 208-210.
- 35 Hayashi, S. and Wu, H.C., 1992, in N.M. Hooper and A.J. Turner (ed.) *Lipid
Modification of Proteins: A Practical Approach*. Oxford University Press,
New York, pp. 261-285.

- Heinkoff and Heinkoff, 1993, *Proteins*, 17 : 49-61.
- Herrera-Estrella et al., 1983, *Nature*, 303 : 209-213.
- Herrera-Estrella, 1984, *Nature*, 310 : 115-120.
- Heyraud-Nitschke, F. et al., 1995, *Nucleic Acids Research*, Vol. 23, N° 6.
- 5 Higgins et al., 1996, *Meth. Enzymol.*, 266 : 383-402.
- Horner, G.W., 1991, *Surveillance* 18(5) : 23.
- Houbenweyl, 1974, in *Meuthode der Organischen Chemie*, E. Wunsch Ed.,
Volume 15-I et 15-II, Thieme, Stuttgart.
- Hueck, C.J., 1998, *Molec. Biology Rev.*, 62 : 379-433.
- 10 Huovinen, P. et al., 1989 *Ann., Intern Med* 110 : 612-616.
- Huse et al., 1989, *Science*, 246 : 1275-1281.
- Huygen, K. et al., 1996, *Nature Medicine*, 2(8) : 893-898.
- Innis, M.A. et al. 1990. in *PCR Protocols. A guide to Methods and Applications.*-
San Diego : Academic Press.
- 15 Inoue et al., 1987, *Nucl. Acids Res.*, 15 : 6131-6148.
- Inoue et al., 1987, *FEBS Lett.* 215 : 327-330.
- Jackson, L.A. et al., 1997 *Am., J. Pathol.* 150. : 1785-1790.
- Jantos et al., 1997, *J. Clin. Microbiol.*, 35(3) : 620-623.
- Kabat E. Et al., 1983, *Sequences of Proteins of Immunological Interest*,
20 U.S. Dept. Of Health and Human Services.
- Kaneda, et al., 1989, *Science*, 243 : 375.
- Kelsey et al., 1987, *Genes and Devel.*, 1 : 161-171.
- Kievitis, T. et al., 1991, *J. Virol. Methods*, 35 : 273-286.
- Kleemola, M. et al., 1988, *J. Infect. Dis.* 157 : 230-236.
- 25 Kohler, G. et al., 1975, *Nature*, 256(5517) : 495-497.
- Kollias et al., 1986, *Cell*, 46 : 89-94.
- Kozbor et al., 1983, *Immunol. Today*, 4 : 72.
- Krone, J.R. et al., 1997, *Anal. Biochem.*, 244, 1, 124-132.
- Krumlauf et al., 1985, *Mol. Cell. Biol.*, 5 : 1639-1648.
- 30 Kuo, CC. et al., 1988, *J. Clin. Microbiol.* 26 : 812-815.
- Kuo, CC. et al., 1993, *J. Infect. Dis.* 167 : 841-849.
- Kwoh, D.Y. et al., 1989, *PNAS. USA*, 86 : 1173-1177.
- Ladany, S. et al., 1989, *J. Clin. Microbiol.* 27 : 2778-2783.
- Laitinen, K. et al., 1997. *Chlamydia pneumoniae Infection Induces Inflammatory*
35 *Changes in the Aortas of Rabbits.* *Infect. Immun.* 65:4832-4835.
- Lazarowitz, S. G. et al., 1989, *The EMBO Journal*, Vol. 8 N° 4 : 1023-1032.
- Leder et al., 1986, *Cell*, 45 : 485-495.

- Lee, C.A., 1997, Trends Microbiol., 5 : 148-156.
- Leininger, E. et al., 1991, PNAS USA, 88 : 345-349.
- Lipshutz, R.J. et al., 1995, Biotechniques, 19(3) : 442-447.
- Liu, H. et al., 1997, J. Gen. Virol. 78(Pt6) : 1265-1270.
- 5 Livache, T. et al., 1994, NAR, 22(15) : 2915-2921.
- Lockhart, D.J. et al., 1996, Nature Biotechnol., 14 : 1675-1680.
- Longbottom et al., 1998, Infect Immunol., 66 : 1317-1324.
- Luckow, V.A., 1993, Baculovirus systems for the expression of human gene products.
Curr. Op. Biotechnology 4 : 564-572.
- 10 Lukacova, M. Et al., 1994, Infect. Immunol. June, 62(6) : 2270-2276.
- MacDonald, 1987, Hepatology, 7 : 425-515.
- Mankertz, A. et al., 1997, J. Virol., 71 : 2562-2566.
- Mason et al., 1986, Science, 234 : 1372-1378.
- Matson, R.S. et al., 1994, Analytical Biochemistry, 217 : 306-310.
- 15 Matthews, J.A. et al., 1988, Anal. Biochem., 169 : 1-25.
- McNeilly, F. et al., 1996, Vet. Immunol. Immunopathol., 49 : 295-306.
- Meehan, B.M. et al., 1997, J. Gen. Virol., 78 : 221-227.
- Mérel, P., 1994, De la PCR aux puces à ADN, Biofutur, 139 : 58.
- Merrifield, R.D., 1966, J. Am. Chem. Soc., 88(21) : 5051-5052.
- 20 Midoux, 1993, Nucleic Acids Research, 21 : 871-878.
- Miele, E.A. et al., 1983, J. Mol. Biol., 171 : 281-295.
- Moazed, T.C. et al., 1997. Murine Model of Chlamydia pneumoniae Infection
and Atherosclerosis. J. Infect. Dis. 175:883-890.
- Mogram et al., 1985, Nature, 315 : 338-340.
- 25 Mordhorst, C.H. et al., 1992 Eur. J. Clin. Microbiol. Infect Dis 11 : 617-620.
- Morrison et al., 1984, PNAS USA, 81 : 6851-6855.
- Morrison, R.P. et al., 1995. Gene Knockout Mice Establish a Primary Protective Role
for Major Histocompatibility Complex Class II-Restricted Responses in Chlamydia
trachomatis. Infect. Immun. 63:4661-4668.
- 30 Murphy, F.A. et al., 1995, Sixth Report of the International Committee on Taxonomy
of Viruses. Springer-Verlag Wien New York.
- Nakai, K. and Kanehisa, M., 1991, Proteins, 11 : 95-110.
- Nielsen, H. et al., 1997, Protein Engin., 10 : 1-6.
- Neuberger et al., 1984, Nature, 312 : 604-608.
- 35 O'Donnell-Maloney, M.J., 1996, Trends Biotechnol., 14 : 401-407.
- Ogawa, H. et al., 1992 J. Laryngol. Oto 106 : 490-492.
- Olins, P.O., and Lee, S.C., 1993, Recent advances in heterologous gene expression

- in *E. coli*. *Curr. Op. Biotechnology* 4 : 520-525.
- Ornitz et al., 1986, *Cold Spring Harbor Symp. Quant. Biol.*, 50 : 399-409.
- Pagano et al., 1967, *J. Virol.*, 1 : 891.
- Peterson, E.M. et al., 1998, *Infect. Immunol. Aug.*, 66(8) : 3848-3855.
- 5 Peterson, E. et al., 1988. Protective Role of Magnesium in the Neutralization by Antibodies of *Chlamydia trachomatis* Infectivity.
- Pierschbacher and Ruoslahti, 1987, *J. Biol. Chem.*, 262 : 17294-17298.
- Pinkert et al., 1987, *Genes and Devel.*, 1 : 268-276.
- Pugsley, A.P., 1993, *Microbiol. Rev.*, 57 : 50-108.
- 10 Puolakkainen, M. et al., 1993 *J. Clin. Microbiol.* 31 : 2212-2214.
- Rank, R.G. et al., 1988. Susceptibility to reinfection after a primary chlamydial genital infection. *Infect. Immun.* 56:2243-2249.
- Readhead et al., 1987, *Cell*, 48 : 703-712.
- Reeves, P.R. et al., 1996, in *Bacterial Polysaccharide Synthesis and Gene*
- 15 *Nomenclature*, Elsevier Science Ltd., pp. 10071-10078.
- Roivainen, M. Et al., 1994, *Virology*, 203 : 357-365.
- Rolfs, A. et al., 1991, In *PCR Topics. Usage of Polymerase Chain reaction in Genetic and Infectious Disease*. Berlin : Springer-Verlag.
- Salzberg et al., 1998, *Nucl. Acids Res.*, 26 : 544-548.
- 20 Sambrook, J. et al., 1989, In *Molecular cloning : A Laboratory Manual*. Cold Spring Harbor, NY : Cold Spring Harbor Laboratory Press.
- Sanchez-Pescador, R., 1988, *J. Clin. Microbiol.*, 26(10) : 1934-1938.
- Sani, 1985, *Nature*, 314 : 283-286.
- Sarver et al., 1990, *Science*, 247 : 1222-1225.
- 25 Schachter, J. 1980. *Chlamydiae*, p.357-365. In E.H. Lennette (ed.), *Manual of clinical microbiology*, 3rd ed. American Society for Microbiology, Washington, D.C.
- Schneewind, O. Et al., 1995, *Science*, 268 : 103-106.
- Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Karlin and Altschul*, 1990, PNAS USA, 87 : 2267-2268.
- 30 Segev D., 1992, in « Non-radioactive Labeling and Detection of Biomolecules ». Kessler C. Springer Verlag, Berlin, New-York : 197-205.
- Sheldon, E.L., 1993, *Clin. Chem.*, 39(4) : 718-719.
- Shiver, J.W., 1995, in *Vaccines 1995*, eds Chanock, R.M. Brown, F. Ginsberg, H.S. & Norrby, E.), pp.95-98, Cold Spring Harbor Laboratory Press, Cold
- 35 Spring Harbor, New York.
- Shoemaker, D.D. et al., 1996, *Nature Genet*, 14 : 450-456.
- Shor, A. et. al., 1992 *S. Afr. Med. J.* 82 : 158-161.

- Sosnowsky et al., 1997, PNAS., 94, 1119-1123.
- Struyve, M. et al., 1991, J. Mol. Biol., 218 : 141-148.
- Sundelof, et al., 1993 Scand. J. Infec. Dis. 25 :259-261.
- Sutcliffe, I.C. and Russell, R.R.B., 1995, J. Bacteriol. 177 : 1123-1128.
- 5 Swift et al., 1984, Cell, 38 : 639-646.
- Takeda et al., 1985, Nature, 314 : 452-454.
- Tascon, R.E et al., 1996, Nature Medicine, 2(8) : 888-892.
- Thom, D.H. et al., 1990 Am. J. Epidemiol 132 : 248-256.
- Thomas, GN. et al., 1997 Scand., J. Infect. Dis. Suppl 104, 30-33.
- 10 Tischer, I. et al., 1982, Nature, 295 : 64-66.
- Tischer, I. et al., 1986, Arch. Virol., 91 : 271-276.
- Tischer, I. et al., 1988, Zentralbl Bakteriол Mikrobiol Hyg [A] 270 : 280-287.
- Tischer, I. et al., 1995, Arch. Virol., 140 : 737-743.
- Tompson et al., 1994, Nucl. Acids Res., 22(2) : 4673-4680.
- 15 Urdea, M.S., 1988, Nucleic Acids Research, 11 : 4937-4957.
- Villa-Kamaroff et al., 1978, PNAS USA, 75 : 3727-3731.
- Wagner et al., 1981, PNAS USA, 78 : 1441-1445.
- Walker, G.T. et al., 1992, NAR 20 : 1691-1696.
- Walker, G.T. et al., 1992, PNAS. USA, 89 : 392-396.
- 20 White, B.A. et al., 1997, Methods in Molecular Biology, 67, Humana Press, Towota.
- Yamamoto et al., 1980, Cell, 22 : 787-797.
- Yershov, G. et al., 1996, PNAS., USA, 93 : 4913-4918.

WHAT IS CLAIMED IS:

- 1- An isolated polynucleotide having a nucleotide sequence of a *Chlamydia pneumoniae* genome, comprising
- 5 (a) the a nucleotide sequence of SEQ ID No. 1;
- (b) the nucleotide sequence contained within the *Chlamydia pneumoniae* genomic DNA in ATCC Deposit No. _____;
- (c) the nucleotide sequence contained in a clone insert in ATCC Deposit No. _____;
- 10 (d) a nucleotide sequence exhibiting at least 99.9% identity with the sequence of SEQ ID No. 1; or
- (e) a nucleotide sequence exhibiting at least 80% homology to SEQ ID No. 1.
- 15 2- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. _____ or to a clone insert in ATCC Deposit No. _____ under conditions of high stringency.
- 3- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. _____ under conditions of intermediate stringency.
- 20 4- An isolated polynucleotide having a nucleotide sequence of an open reading frame (ORF) of a *Chlamydia pneumoniae* genome, comprising:
- 25 (a) a nucleotide sequence chosen from one of ORF2 to ORF 1297;
- (b) a nucleotide sequence exhibiting at least 99.9% identity with one of ORF2 to ORF 1297; or
- (c) a nucleotide sequence exhibiting at least 80% homology to one of ORF2 to ORF 1297.
- 30 5- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of high stringency.
- 6- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of intermediate stringency.
- 35 7- The polynucleotide of Claims 2, 3, 4, 5, or 6 which encodes the following polypeptides or fragments thereof:
- (a) a *Chlamydia pneumoniae* transmembrane polypeptide having
- 40 between 1 and 3 transmembrane domains;

- (b) a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;
- (c) a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;
- 5 (d) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;
- (e) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;
- 10 (f) a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;
- (g) a *Chlamydia pneumoniae* polypeptide having involved in metabolism of fatty acids;
- (h) a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;
- 15 (i) a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;
- (j) a *Chlamydia pneumoniae* transport polypeptide;
- (k) a *Chlamydia pneumoniae* polypeptide involved in the virulence process;
- 20 (l) a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;
- (m) a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae*.
- (n) a *Chlamydia pneumoniae* surface exposed polypeptide;
- 25 (o) a *Chlamydia pneumoniae* lipoprotein;
- (p) a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;
- (q) a *Chlamydia pneumoniae* KDO-related polypeptide;
- (r) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;
- 30 (s) a *Chlamydia pneumoniae* lipid A component-related polypeptide;
- (t) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;
- 35 (u) a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;
- (v) a *Chlamydia pneumoniae* Type III secreted polypeptide;
- (w) a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or

- (x) a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

8- A polynucleotide encoding a fusion protein, comprising one of ORF2 to ORF1297 of
5 Claim 4, 5, or 6 ligated in frame to a polynucleotide encoding a heterologous polypeptide.

9- A recombinant vector that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

10- A recombinant vector that contains the polynucleotide of Claim 8.

10

11- A recombinant vector that contains the polynucleotide of Claim 4, 5 or 6, operatively associated with a regulatory sequence that controls gene expression.

12- A recombinant vector that contains the polynucleotide of Claim 8 operatively associated
15 with a regulatory sequence that controls gene expression.

13- A genetically engineered host cell that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

20 14- A genetically engineered host cell that contains the polynucleotide of Claim 8.

15- A genetically engineered host cell that contains the polynucleotide of Claim 4, 5 or 6 operatively associated with a regulatory sequence that controls gene expression in the host cell.

25

16- A genetically engineered host cell that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression in the host cell.

17- A method for producing a polypeptide, comprising:

30

- (a) culturing the genetically engineered host cell of Claim 15 under conditions suitable to produce the polypeptide encoded by the polynucleotide; and
- (b) recovering the polypeptide from the culture.

35 18- A method for producing a fusion protein, comprising:

- (a) culturing the genetically engineered host cell of Claim 16 under conditions suitable to produce the fusion protein encoded by the polynucleotide; and
- (b) recovering the fusion protein from the culture.

19- A polypeptide encoded by the polynucleotide of Claim 4, 5 or 6.

20- The polypeptide of Claim 19 which immunoreacts with seropositive serum of an
5 individual infected with *Chlamydia pneumoniae*.

21- The polypeptide of Claim 19 which comprises the following polypeptides or fragments thereof:

- 10 (a) a *Chlamydia pneumoniae* transmembrane polypeptide having between 1 and 3 transmembrane domains;
- (b) a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;
- (c) a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;
- 15 (d) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;
- (e) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;
- 20 (f) a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;
- (g) a *Chlamydia pneumoniae* polypeptide involved in metabolism of fatty acids;
- (h) a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;
- 25 (i) a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;
- (j) a *Chlamydia pneumoniae* transport polypeptide;
- (k) a *Chlamydia pneumoniae* polypeptide involved in the virulence process;
- 30 (l) a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;
- (m) a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae*.
- (n) a *Chlamydia pneumoniae* surface exposed polypeptide;
- 35 (o) a *Chlamydia pneumoniae* lipoprotein;
- (p) a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;
- (q) a *Chlamydia pneumoniae* KDO-related polypeptide;

- (r) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;
- (s) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;
- 5 (t) a *Chlamydia pneumoniae* lipid A component-related polypeptide;
- (u) a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;
- (v) a *Chlamydia pneumoniae* Type III secreted polypeptide;
- 10 (w) a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or
- (x) a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

15 22- A fusion protein encoded by the polynucleotide of Claim 8.

23- The fusion protein of Claim 22 which immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

20 24- An antibody that immunospecifically binds to the polypeptide of Claim 19.

25- An antibody that immunospecifically binds to the fusion protein of Claim 22.

26- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological
25 sample, comprising:

- (a) contacting the sample with a polynucleotide primer of Claim 1, 2, 3, 4, 5, or 6 in the presence of a polymerase enzyme and nucleotides under conditions which permit primer extension; and
- 30 (b) detecting the presence of primer extension products in the sample in which the detection of primer extension products indicates the presence of *Chlamydia pneumoniae* in the sample.

27- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological
35 sample, comprising:

- (a) contacting the sample with a polynucleotide probe of Claim 1, 2, 3, 4, 5, or 6 under conditions which permit hybridization of complementary base pairs; and

- (b) detecting the presence of hybridization complexes in the sample in which the detection of hybridization complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

5 28- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

- (a) contacting the sample with the antibody of Claim 24 under conditions suitable for the formation of immune complexes; and
- (b) detecting the presence of immune complexes in the sample, in
10 which the detection of immune complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

29- A method for the detection and/or identification of antibodies to *Chlamydia pneumoniae* in a biological sample, comprising:

- 15 (a) contacting the sample with a polypeptide of Claim 19 under conditions suitable for the formation of immune complexes; and
- (b) detecting the presence of immune complexes in the sample, in which the detection of immune complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

20

30- A DNA chip containing an array of polynucleotides comprising at least one of the polynucleotides of Claim 1, 2, 3, 4, 5, or 6.

31- A protein chip containing an array of polypeptides comprising at least one of the
25 polypeptides of Claim 19.

32- An immunogenic composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.

30 33- An immunogenic composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.

34- An immunogenic composition comprising the fusion protein of Claim 22 and a pharmaceutically acceptable carrier.

35

35- An immunogenic composition comprising the fusion protein of Claim 23 and a pharmaceutically acceptable carrier.

- 36- A pharmaceutical composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.
- 37- A pharmaceutical composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.
- 38- A pharmaceutical composition comprising the polypeptide of Claim 22 and a pharmaceutically acceptable carrier.
- 39- A pharmaceutical composition comprising the polypeptide of Claim 23 and a pharmaceutically acceptable carrier.
- 40- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 32.
- 41- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 33.
- 42- A method of immunizing against *Chlamydia pneumoniae*, comprising administering to a host an immunizing amount of the immunogenic composition of Claim 34.
- 43- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 35.
- 44- A DNA immunogenic composition comprising the expression vector of Claim 11.
- 45- The DNA composition of Claim 44, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae*.
- 46- A DNA immunogenic composition comprising the expression vector of Claim 12.
- 47- The DNA composition of Claim 46, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae*.
- 48- A screening assay, comprising:
- (a) contacting a test compound with an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6; and
 - (b) detecting whether binding occurs.

49- A screening assay, comprising:

- (a) contacting a test compound with the polypeptide of Claim 19;
and
- (b) detecting whether binding occurs.

5

50- A screening assay, comprising:

- (a) contacting a test compound with the polypeptide of Claim 22;
and
- (b) detecting whether binding occurs.

10 51- A kit comprising a container containing an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

52- The kit of Claim 51 wherein the polynucleotide is a primer or a probe.

15 53- The kit of Claim 51 wherein the polynucleotide is a primer and the kit further comprises a container containing a polymerase.

54- The kit of Claim 51 which further comprises a container containing deoxynucleotide triphosphates.

20

55- A kit comprising a container containing an antibody that immunospecifically binds to the polypeptide of Claim 19.

56- A kit comprising a container containing an antibody that immunospecifically binds to the
25 fusion protein of Claim 22.

Figure 1.

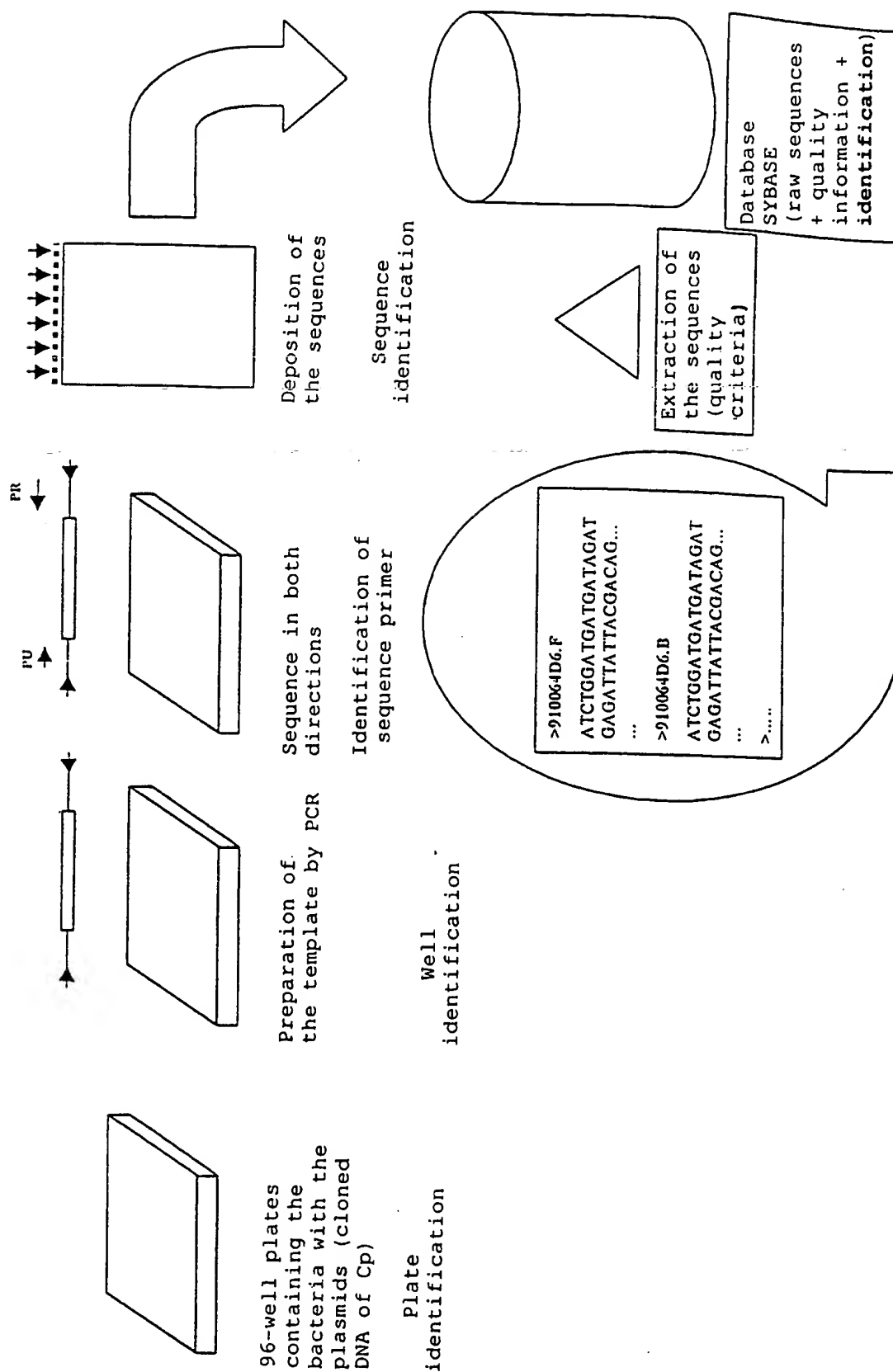


Figure 2.

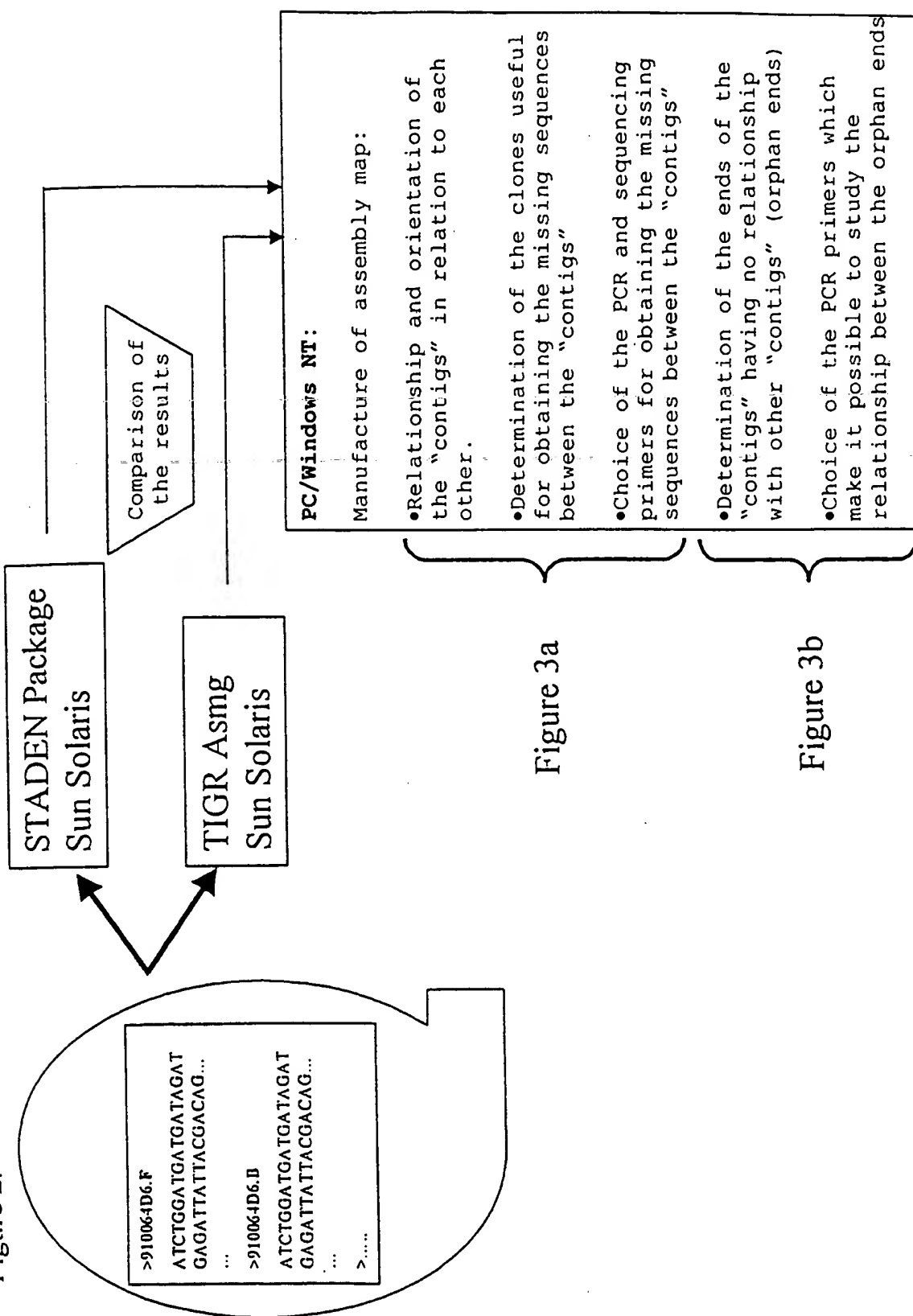


FIGURE 3A



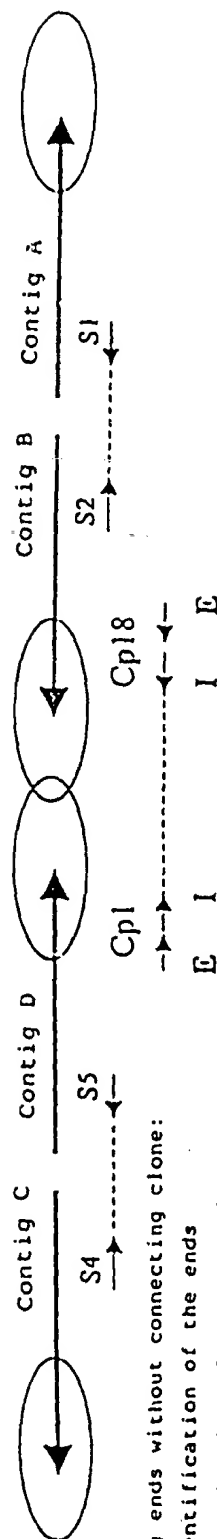
Distribution and position of the sequences on the contigs:

- 1- Define the arrangement of the contigs in relation to each other
- 2- Define the PCR primers which make it possible to fill the sequence

Statistical determination of the sequences:

- 1- Belonging to the same clone
- 2- Situated on two different contigs

FIGURE 3B



Contig ends without connecting clone:

- 1- Identification of the ends
- 2- Determination of outer and inner PCR primers for studying the relationships between the contigs

E: outer primers

I: inner primers

SEQUENCE LISTING

<110>Genset SA

<120>Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

<151>1997-11-21

<160>6849

<210>1

<211>1230025

<212>DNA

<213>Chlamydia pneumoniae

<400>1

atagaaaact	attaaaaaat	cattgattct	gtcgggaaag	tatgcggata	aaattcagag	60
agaataagga	gaggaagatg	acaaggcaga	gttatgtttt	gggcaattgg	aaaatgcaca	120
aaacaatcca	agaagctaaa	gagtatgttc	aaacattagc	ttctntacta	caaggagaac	180
ctctttcctg	cactataggc	atagcttctc	cattttacctc	tttgagagcg	attcatgaga	240
tgataaacac	tacgggagct	ttctctctgt	tgggagcaca	aaatgtccat	cccagagctt	300
cgggtgcttt	tactggagaa	atttccttac	ctatgcttaa	ggaggttaga	gtggaatttg	360
tttttagtagg	tcactccgag	cgctgctcata	tttttggaga	gagtgatgcc	tttattgctt	420
caaaggtaaa	gtctgtagct	caggcgggac	tctgtgctgt	tctttgtgtt	ggagagagct	480
tagaagttcg	tgaagaggga	aaggcgcctc	aggtaatcaa	aaaacagttg	cttttgggat	540
tggaaacagat	ggataatggt	tccgaatttt	tgatcgcccta	tgaaccagta	tgggctatcg	600
gcacagggaa	ggtggcagaa	gcttcggatg	tgcaagatat	tcatatgttt	tgtcgtgagg	660
tagtggcaga	gaggttctca	gaagctacag	ctgaagagat	ttcgattttg	tacggaggat	720
ctgtgaaggt	cgataatgct	cagcgatttg	ggcaatgtag	cgacgtcgat	ggtcttttag	780
ttggcggant	tcttttagang	ggcaaagtgt	ttttgaagtc	gctaaaaatt	ttaatgtata	840
atttgtgaga	gttatgagat	ttttttgtct	attttttctt	gggttcctag	gatcttttca	900
ttgtgttgct	gaagacaagg	gcgtggattt	atttggagtc	tgggacgata	accaaattac	960
agagtgtgac	gatagttaca	tgacagaggg	tctgtgaagag	gttgaaaagg	tagtggacgc	1020
ttagtccatt	ggcttttatt	tatattctcc	ctaagggaag	cctgtattga	agatcgcttt	1080
ctcatagata	gaagtaattt	tcagatagtc	aataattggt	ttttttaaga	gaatgctagg	1140
caggtgctcg	tgtttgggca	tttgattaag	tctacatgaa	tctggaggga	gagattcttc	1200
tggtattgag	aagtagaaca	aaaaacaagg	atcagacgtt	ctccgatgtc	ttcctaateg	1260
atgtctttta	ataaggagat	tggcatgaca	gtgttggttt	acgcattttt	attcattttc	1320
ctttttctat	gtgtaattct	ttgtggctta	atcctgggtc	aagagagtaa	gagcatgggg	1380
ttaggttctt	cgttcggcgt	ggattctgga	gattctgtct	ttggtgtctc	tactccagat	1440
attttgaaaa	aagtgacttc	atngtgtgct	gttgctttct	gcataggttg	tttactactt	1500
tcattttcca	cgaaatctct	ggggaaaaag	ttagatgcta	aagaatttct	attgcctgct	1560
gctgaggaga	gcgacactca	agcttcttct	gagagcgttg	aagcagatga	atcctagcct	1620
atttgcggaa	ttagggtgtg	tctagattga	agtgcataaa	agctagcaag	tttttatctt	1680
catacgagat	atgagtgtac	ggtcggataa	gagtagaaat	ctttcttttg	ttcctatggt	1740
taagaagtcc	tttggtcttc	ttaaagagta	tgactcttat	caacccaaga	aatgttttag	1800
atccaagtgc	ttgtcgtacg	agatttcttc	acagagctct	gccaaagcca	tgttcagact	1860
atgattagac	tttagaata	ttacggcagt	cctattttta	ggaaaaagtc	ttcccaatt	1920
gcagagatca	cagatgagat	tcgtaatctc	gtgagtata	tgtgtgatac	tatggaagca	1980
catcgtggtg	tcggttttagc	cgctcctcag	gtagggaaaa	acgtcagttt	atttgtcatg	2040
tgtgtagata	gagagactga	ggatggagag	ttgattttct	ctgagtctcc	gagggatatt	2100
atcaatcctg	ttctatcaga	tccttctgaa	accccgatca	taggtaaaaga	aggatgtctt	2160
tctattcctg	gattgcgagg	agaagtattc	cgccctcaga	aaatcacagt	gaccgctatg	2220
gatctcaatg	gtaaaatatt	tactgagcac	ttggaaggat	tactgcacg	tatcattatg	2280
cacgagactg	accatctgaa	tggagtcttc	tatatgtatc	ttatggaaga	acccaaagat	2340
cctaaaaaat	ttaaagcctc	tttagagaag	atcaaacgtc	gctacaatac	acacttgagt	2400
aaagaagaac	tagtttctta	attgtctctc	agtctgatgt	aggtgatatt	ttcttgtctc	2460
ttgcgtcaca	tttgtgtgca	gctttgctta	tttccccgaa	caaatttcgt	caaagggttt	2520
aaaatgtgtc	ttgctgattt	ttgctaagag	ctctttccct	cgttgcttag	cgatctctct	2580
tcctgtctgt	ttgacattga	atccagcacc	tttaggaagc	tgtacttgat	attgttcttc	2640
caacttctgt	atcgactgta	caaatgcctc	tctagccaat	atagaagctg	ctgctacgac	2700
tacatcttgt	tctgcacgtg	gcttttgtat	taaagtaata	tcggtttctt	ttttttgaag	2760
tgctttgagt	aggtgttatt	ctgaagctgc	aaactgatct	gaaatagcaa	agacatctcc	2820
tgcaggtttg	ggtgctaagt	tgttgataac	agtagcgtgg	gccccagcaa	gaagtgtatt	2880
taaattctgg	aatttcccat	atagctcggt	atatttttct	gggtatagaa	tgatgacatc	2940
gcagacacat	agtgagcgta	tgatacgtgc	taaagaagcg	attttcgtgt	ctttgagatt	3000
tttagagtct	tggactttat	tctcatagag	tttttttaag	atctctgcat	tcgatgcata	3060
gactgccgca	atacataaag	ggccaaaaaa	atcacctttc	cctgattcat	cgactcccaa	3120

ccttggacga	aggctcttgc	ctacccttgc	atgggtgaag	gtatgaagga	tttctgggtc	3180
taagaaaaat	tctatgaatt	cctcacttcc	tttaccttgg	attacgagtt	tcccgagggg	3240
gtatagagt	caggtaacag	tggttagagcg	agcttgaaat	acgggtattct	gtggctgaga	3300
aaagataaaa	tttttttctt	ttagctgac	tcttaaatg	ttttgagcag	aagttgttaa	3360
agtaacaaca	aatgggtggcg	gcatgcagga	catctaccta	taaattatag	aaaaaattta	3420
gaacgattga	attcctagtc	ctaggaatcc	aggatgcaaa	gtgctcatac	tttttatttt	3480
tgccactat	atcgtatagt	tatgacaact	tccaagtaca	aattaaacaa	caattttgtg	3540
tattttctgca	aataactgcg	gggagccaaa	gatacaagag	tgtaagatgt	ctagtatttt	3600
acattcttaa	ggttttgaga	aacactatat	aggtaatcat	gcaagaacac	atacataaag	3660
aattgtctaca	tctaggtgaa	atctttcgct	catcacgaga	gtctcaatcc	ctatcgttaa	3720
aggatgtaga	tgctgcaacc	tcgatacgat	atagttgttt	agaagctatt	gaacaggggt	3780
gtttaggaaa	attgatttct	ccagtttatg	ctcagggatt	tattaagaaa	tacgctacgt	3840
atcttgggtt	ggatggagat	agtatcttac	aagaacatcc	ttatgtcatg	aaaattttta	3900
aagagttttc	agatcataat	atggagatgc	tttttagacct	tgaatcgatg	ggaggaagga	3960
attctccgga	aagagcaatt	cattcttgg	cgaatctttg	gtgggcaggg	ctgatcatta	4020
taggtggcat	catggtgtgg	tggtctggat	cgttgttttc	tatttttta	cttaaggtct	4080
gttggctctc	atttagacca	acagatagga	tgagtagtct	cttaccctaa	tttgaatagt	4140
tgtgagactt	tctgagcccc	ttgcaaaagt	tgcttttgat	tttcaggaga	ccagggatct	4200
tcatccctac	cctcatcatc	ctcaggacct	aagggtctctc	ctaaaccatc	acttctctgt	4260
gtactatcac	agccatcgg	tcggctctct	ctctgttggg	agcttctctc	aacaccgaag	4320
gcactggcat	ggaatgccaa	atcctccgcc	tgtcacaata	ccatctcttt	ctattctcg	4380
gtcatccac	gggtcaggag	gtggtggagc	ttgtctagga	gcttcgcctt	gggtttgtct	4440
ccaaatgttc	tctccagctg	tggtgggtgac	taataccttt	ctaagaattc	tttgcaagg	4500
accttggact	ctaggggtcaa	gaacagtttg	ctctggatgt	agaggatcta	aaggaagata	4560
tctttttgaa	agaaggcata	gaaggacaag	gacttcaaat	acctgagatt	ctaaactcaa	4620
accaatacca	ggacctaa	aagtgcgaag	atcactggca	acaagtcttt	ttagtatttt	4680
ttttattaag	tccacaattt	gttttagcagc	ttgtcctaaa	ggacccttgt	aaccggattc	4740
taagctcaaa	acctctaacc	tggataat	ttgtaataaa	gtcctaaaat	tgagtttgca	4800
tgtaacacgg	cattcttgag	cggggtgctt	cttttgttga	ggagctggcg	cgcctcctac	4860
agcaccttgt	agctgttctt	cgtctgttgg	agggtgggga	cagggttgct	gttctgggtg	4920
tagaattcaa	caagtaggag	gattgtcaga	tgaagttaca	aaggaaaagag	ccccctctga	4980
aacagcttga	agtagagac	tccatgggtg	tgctgttgc	atgtcttcgc	ctaagccggt	5040
gttttgtaaa	agcttgacta	gagattcacc	catgcattct	ggttgagctg	cttttagtag	5100
ttcccgatgt	agcttgcaac	cattttcaac	ctcctgttta	tccccgtcac	ccaacggttc	5160
accttgctca	atcttctgtg	tacagtgcgg	tagctgttgg	aaagacatac	caacacaaat	5220
agggtccgtat	tgctgtataa	gttgtttag	aaattgtgct	gagggattat	caggatcatc	5280
cacggtctct	aagcagcatg	cgcaacatcc	tccccatctc	cattgtaaga	aaccaggaca	5340
atgtctctct	caccagggag	tcccggttct	ataacaataa	tgctctagac	gttgcatctc	5400
agcactatct	aagagattat	taagtaacga	gcctgcttgt	tctaccatac	ctagcacatt	5460
gtctgatccg	agcgagatac	ccatttcacg	acctccagtc	ccaggctgtt	gtgtaattac	5520
acgtccacct	tgagagccag	attggcctcc	ttcttgtagt	ggaatatctt	ctcctccggg	5580
atttgggtggg	ggcggttctg	gataataaca	attacaat	ccacatggaa	atgtcatgag	5640
gcttctcctt	tagtgagggt	gagttgtatg	gatttttata	attacgagtt	cttctagaaa	5700
ggaattatag	aatgttcaga	tagagtattt	taaagcgggt	tatttcttat	tggaatgatta	5760
agaaaaatag	gaaatcttga	ttatgttttt	ttgtcgagat	tacttttaga	gaaagagttt	5820
aaagtgtatcg	cgggttatta	gtcaat	tttttaattt	aacatagatc	ctctcttaag	5880
tttctctgtt	gtgatgggat	aaatat	ggaagaaatg	ccgcaaaatt	ttttctaagt	5940
tctcaaaact	ttcaagaaaa	catagattct	tggaatagaac	aaaagcttcg	cggcaaaaaa	6000
taggaatctt	attctttgtt	tattttttatc	cctaaaaata	gagtttgtaa	atgacccgag	6060
cattcaagga	tacgtgtt	atacgccaaa	ttcccatcct	catcatcatc	ttcattttca	6120
tcttcttctt	cgagacttga	catgagaggg	acagattctg	caggggtagg	acaatcaaga	6180
cttctctgtc	ttactaatga	gggtttcttt	tttaaaaacg	atgctgaagt	tttccctgtt	6240
ctatagctgt	attgtagtcg	atagaagatg	gtcataatcg	gatcatctat	catgtgtata	6300
tctacgacag	atgtctcatc	ggtatttgca	gggcaatagc	caatcgctaa	catcaataaa	6360
acgacgatat	cacgaaaatt	tgggcacgta	taacatattt	ctccacctgt	gtgctttaga	6420
atagaagatg	tgctttgtga	tgagataag	agaagctat	tcagcatttt	cacaatcagg	6480
agaccaaaag	gacctaaagc	tgaaaaatct	cctgttttta	gattgggtgac	ttggattttt	6540
cctaattgtc	tgcccatg	attgtcattg	tattttttttg	ctacgtactg	gggctctgca	6600
ccgactgaag	atgggcgtcg	cgcattctct	gatccacagg	ataggcgtga	cgtcgttaag	6660
gggctcgtat	ttaaagata	gcacgcagga	atgcctgtag	aattagaagc	agaagatgtt	6720
cctgaggctt	cctctgat	tatagttttt	tccaagacc	ttgtagcaat	aaagcttagc	6780
acggcttggg	ctagtgaatc	gtctagaccg	cgttctctaa	tgctgttgac	tccttcaagg	6840
aaaaagtttt	gagaaaggct	ctgcacgtt	ccatagagct	gggttttagc	ttccgagcaa	6900
tgctgtctaa	attcattttt	ctgttcttca	gacaaaatag	tgtttttttc	tacaagttcc	6960

atgaagttga	ggcccatagt	tttagcagct	aaagcaacgg	caataggacc	atgggtctgt	7020
tcgcattcat	ggacaagtcc	agcaacctga	ttatcctctc	tgtctaagca	acacgcttta	7080
tacgttccac	aaatgagtct	tccaaaagat	ccgcaacgct	gaccacatcc	agttgcgtaa	7140
ctgtcataac	aatactctgt	acatccttgc	gttcgtctat	gtgatagaat	ggagtctacc	7200
aattctcctg	cttcttggtat	catgtgtatt	gtactttcat	caccttgagc	agtattaaat	7260
tggacacgtt	tctctacttt	tgtaatTTTA	gtaggttgcg	tagttatagg	agcagctcct	7320
ccactcgaac	cagcttcttc	gcttatatct	gaagccgatt	gccgcgttgt	ttcttctgtt	7380
gttggtactt	caacccattc	gcagttgaaa	ttccacacac	ttctgaacca	agaattattt	7440
gggcaaacca	tagtctgacc	tttttaatat	ttagatttat	ttaggtttta	gagagttgaa	7500
aagaactctc	taagaacagg	aaaagagtcg	gtatgctctg	cttgcgactg	tgtcttttgg	7560
aatgggaaac	gaagggtacc	cagtgcttat	agcacagtag	agtgaggcta	aacgtcaaaa	7620
ttgatttgaa	gaaatttgaa	ttgctgacaa	gagggggaga	ggaattaaaa	acgtcggacg	7680
gaagaagatg	tttagagcat	gtataaagaa	aattttaaat	tagatgcatt	atttcatggg	7740
tcttacctta	tttagactta	agatggtaag	gaagtctata	aaatcatttt	ttttaaaatc	7800
tacggaattt	aaaaaattac	ttgataatga	tgtggagtcg	tagaagtgca	aactcactag	7860
aaatttctcg	aatttgagaa	ggagtttaaa	ataggtattc	ttgaaaagat	caatgcacgt	7920
gtagtggaaa	gaaaggcgta	acctacactg	gaaggagttt	cttttagaag	aaggtttctt	7980
ttttcgttgt	taatgacaaa	aactctctaa	gaacatcggt	tcaaccgttt	ttattgttgt	8040
gtttatttaa	aaaaaagatt	atatccttca	tgcaaatTgg	tgctgttgga	aacaaatgtt	8100
gaaaatccag	aaaaaaagaa	tgtgtgtcag	cgtagtcatc	acggtaggcg	ccatagtggg	8160
gtttttcaat	tctgcagacg	cagcaccaaa	gaaaaagaag	atccctatac	agattctcta	8220
ctcctttact	aaagtctctt	cctattttaa	aaacgaagac	gcaagtacta	tattttgcgt	8280
cgatgtggat	cgtggacttc	tccagcatcg	gtatttaggt	agtcaggat	ggcaggaaa	8340
cagacgtcgg	cagttattta	aatccttaga	aaatcaatca	tacggcaacg	aacgttttag	8400
agaagaaact	cttgctattg	atattttcag	gaacaaagag	tgcttgagga	gcgagatccc	8460
agagcagatg	gaagctatcc	ttgcaaatc	ctcggccttg	gtcttaggca	tctcttcttt	8520
tgggatcaca	ggaattcctg	cgactttgca	tagtttgctt	cgacagaatc	tatctttcca	8580
aaaacgctct	atagcatcgg	agagcttcct	tttaaagatc	gatagtgcgc	cctcagatgc	8640
ctctgttttt	tataaaggcg	tgcttttccg	cggagagact	gcgatcgtgg	atgcgttaag	8700
ccaattattt	gccagctcgg	atcttttctc	taaaaaaatt	atctttctag	gagaagacc	8760
tgaggtcggt	caagctgttg	ggtctgcttg	tataggttgg	ggcatgaact	ttttaggcct	8820
ggtactatat	cctgtcaag	aaagcctttt	ttcttatgtt	catccttact	ctacagcaac	8880
ggagctccaa	gaagcacagg	gtttacaagt	aatttcagat	gaagtcgcac	agcttacttt	8940
aaacgctctt	ccgaaaatga	attaacatga	tgtagaaca	acaagcccta	cgtattctct	9000
ttccccctga	gggtgcttag	ggcccttttt	atctagcatg	agcggagatt	taggttttag	9060
tgagattttt	ggtaaatatg	aaaatatTTT	cttaaaaaaga	tcatgaaaca	gtcatacttt	9120
tgcattgaag	gatctttatg	agacgttatc	ttttcatggt	tctagcttta	tgccatatata	9180
gagcagcccc	tctcgaagca	gtggtcatta	aaattactga	tgcgacaggca	gttcttaagt	9240
ttgctagaga	gaaaacttta	gtatgtttca	atattgaaga	tactgtggta	tttcttaaac	9300
agatggctcg	ccagtctgca	tggctctaca	atagagagct	cgatcttaag	actacactct	9360
ccgaagaaca	agccagagag	caggcgcttc	tggagtggat	ggggatttct	tttcttgctg	9420
attatgaatt	ggtgagcgcg	aacttaagga	atgtactcac	aggcttatct	ttgaaacgat	9480
cttgggtact	cgggatttct	caaagacctg	tgcatttgat	aaaaaatact	cttcgcattc	9540
tgcgttcttt	caacatagac	ttcacctcgt	gtccagctat	ttgtgaagat	ggttggtctt	9600
ctcactcttc	aaaggacaca	acattcgtac	agccatggc	tatagaaaaa	aacattttgt	9660
ttgttggtct	tctcaaaaac	ggctcagccca	tggacgcagc	ccttgaagtt	cttctctctg	9720
ggatctcttc	tctccttagc	caaactcatc	atgtggatca	ggatgcagaa	cgtttgcggt	9780
ctatcgggtg	tttttgtaaa	aaagcaaaaca	tttattttat	agggatgctc	tacaccccag	9840
ccaagcagcg	tgtagaaagt	tacaatccta	aacttactgc	gatccaatgg	tcgcagattc	9900
gtaagaatct	ttccgatgaa	tattatgaat	ccctcttgag	ctatgtaaag	agcaaagggt	9960
agtgtcagca	aatcgatgtg	ggaatgggtat	cctgtggatg	gcatagacac	gcaaggcggt	10020
ttttatgccg	tttttagatc	cttgtagggtg	cagaaaaact	aaaaagatcg	gaagagaagg	10080
gattcgaacc	cctgggttct	gtaagagaac	ttctgatttc	gaatcagacg	catttcgacca	10140
ctctgccact	cttcgcgtat	gcttcaatag	tttagagaat	ctacactcag	attgtctaca	10200
tgtattgcac	aatgtttttc	ataaatTTT	gaaatcataa	tgaagattag	agaagatggc	10260
cgagtagtga	agacgaattc	ttagagaaaa	attagagtgt	tttcttgctg	atctaggcag	10320
aaaactaccc	tcaagaagag	gcttgagggtg	gaaacatcta	atTTTTgtca	gaatgatgag	10380
agtggcagcc	tcttgaagag	cagctgtctc	cgtgtgaatg	acgggacttc	ttgctgcaga	10440
aaggacaaaa	gcttagcaag	caaatgacac	cagcaattcc	aatgataata	taggtaattt	10500
gggtggcagg	agttagaaacg	cctccacaca	acttagcaat	aatattttaa	ttattgtgag	10560
tgattccttat	aagttccacg	ttcaatgcac	aaagaataac	aataagagag	gataatcctc	10620
gaataatttt	gcctagcatc	gcttttctcc	taagtgtatg	atacttaatt	tcatctttta	10680
atctttttta	taatttaata	aacagttttt	ttcaaaagac	ttctttgcta	aagtctctca	10740
gtctcgttga	ctttttgaat	acaaagggtt	aagttgttca	agaagttttt	gaactgtaaa	10800

daacttccag	tttttatgat	tagagagaca	gttcagaata	aaaacttcaa	ttttttaagt	10860
ttagataatc	tttctttact	tgcattgaga	aaagagcata	tttttataag	ccgcaattta	10920
ggataacata	tggagcaatt	tcatttggat	agggagaana	ttttactttt	ggcaaaggcc	10980
tcagcactac	aactttctga	agagcttata	caggagtata	aaacttcttt	aagcgtgtgt	11040
attacttcta	tgaagaagc	tcttgccata	gagattgatg	atgcggattc	atgcgaatct	11100
ctttttatgc	atgtagtaaa	tgttgaagat	ttgagagaag	attcggtgac	ctctgatttc	11160
aatcgagagg	aatttttgcg	taatgttcca	gagtccttag	ggggattagt	gaaagtccct	11220
gcggtaatca	agtaaggag	tctgaaaaat	tatgtatcga	tatagtgtct	tagaatttagc	11280
aaaagctgtg	acttttagggg	aactgacagc	cacagggtgt	actcaacatt	tttttcatag	11340
aatagaagaa	gctgaggggc	aggtaggtgc	ctttatttcc	ttgtgtaagg	aacaagcttt	11400
agaacaggca	gagctcatag	ataaaaaagc	ttcgctgga	gaacctttag	gaaaaactgc	11460
agggttctct	ttaggaatta	aagataatat	tcacgttaca	ggcctgaaga	caacatgcgc	11520
ctctcgtgtg	ctcgagaatt	atcaaccacc	gtttgatgct	actgtttag	aaagaatcaa	11580
aaaagaagat	gggattatct	taggcaaact	caatatggat	gagtttgcta	tgggatcaac	11640
aacgctatat	tctgtctttc	atcctacca	caaccctgg	gatttatctc	gtgttccctgg	11700
aggttcttca	gggggatctg	cggccgcagt	ttctgctaga	ttttgtcccg	tagccctagg	11760
atcagatacc	ggaggatcca	tccgtcagcc	cgcagcattt	tgtggtgttg	taggttttaa	11820
gccttctac	ggagccgttt	cgcgttacgg	gttgcctacc	tttgctctct	cgctagatca	11880
aatcggctct	ttagccaata	ctgtagaaga	cgctgccta	atgatggatg	tgttttctgg	11940
tagagatcct	aaagatgcaa	cctcaagaga	gtttttccgt	gattctttta	tgagcaagtt	12000
gtctacggag	gttcttaag	tgattgggt	gcctagaaca	tttttagagg	gactccgtga	12060
tgatattagg	gagaatttct	tctcttcatt	agccattttt	gaaggagaag	gaaccatct	12120
tgtggatgtg	gagttggata	ttctcagcca	cgctgtatct	atataattaca	ttttagcatc	12180
tgtgaagct	gccacgaatt	tagcaaggtt	cgatgggtgt	cgttatggat	atcgttctcc	12240
tcaagcgcat	accatcagcc	aactctacga	tctctcacgt	ggagaaggat	ttggcaaga	12300
ggctcatgct	agaatcctct	tagggaacta	tgtcttgtct	gcggagagac	agaatgttta	12360
ttataagaaa	gctacggcag	tgcgtgctaa	gattgtaaaa	gcatttagaa	ctgcatttga	12420
aaagtgtgaa	atcttagcca	tgcctgtctg	ttctagcccc	gcgtttgaaa	taggagaaat	12480
tctagatcct	gtgactttat	atctacagga	tatctatact	gtagctatga	atttagcgta	12540
tcttccctgcc	attgccgtac	cctctggatt	ttctaaggag	ggcctgccct	taggcctaca	12600
gattatcgga	cagcaaggac	aagaccaaca	agtgtgcaa	gtgggttaca	gtttccaaga	12660
gcatgcgcaa	attaagcaat	tgttttctaa	gagatatgcc	aaaagtgttg	ttctaggagg	12720
tcaatcatga	tgctgtttta	tgcagatttg	gaatcagtc	taggacttga	agttcacgta	12780
gaattgaaca	cagcatccaa	gttattttagc	tctgctttaa	atcgctttgg	agatgaacca	12840
aacactaata	tttctacagt	atgtacagga	ttgccaggat	cattgcctgt	attgaatcag	12900
agtgcctgtg	agaaagctgt	gctttttggc	tgcgtgtctg	aagggtgaaat	ctctctattg	12960
agtcgtttcg	ataggaagtc	ttacttctat	cccgatagtc	ccaggaattt	tcaaattaca	13020
caattcgaac	atcctattat	ccgaggagga	cgcattaagg	cgattgtcca	aggggaagag	13080
cgttatatttg	aattagccca	aacctatata	gaagatgatg	ccggaatgct	gaagcacttc	13140
ggagagtttg	ccggtgtaga	ctacaatcgt	gccggagtcc	ccctaatacga	aattgtttca	13200
aaacctgtga	tgttttgtcc	tgaagatggc	tgttgttacg	caacttcttt	ggtttccctg	13260
ttagactata	ttggaatttc	cgattgcaat	atggaagaag	gtccatccg	ttttgatgtc	13320
aatgtctccg	tacgccctaa	gggatcccca	gaacttcgca	ataaggtaga	aatcaagaat	13380
atgaactcct	tcgcttttat	ggcacaagct	ttagaagctg	aaaaacaacg	tcagatcgat	13440
gagtatctta	atcagccaaa	taaagatccc	aagctgggtga	ttccagccgc	tacctaccgc	13500
tgggatcccc	aaaagaaaaa	aactgtgtct	atgcgtctca	aagagagtgc	cgaagattat	13560
aaatattttc	ccgagcctga	tctgccgaca	ctacaattga	cagagtccta	tatagaaagg	13620
attcgcaaga	ccttgccaga	acttccctat	gacaagtacc	atcgctatat	tcaggagtac	13680
ggtctatccg	aagatatcgc	aagtattctg	atcagcgata	agaatatcgc	aacgtttttt	13740
gaagtgcgtt	gtaaaagattg	taaaaaacttt	aggcttttat	ctaactgggt	aaccgttgaa	13800
tttgaggggc	gctgcaaaac	cctaggagtgt	aagttgacct	cttcagggaat	tttccccgag	13860
ggagtgcgtc	agctgggtcaa	cgcaatcgac	caaggtgtga	tcacagggaa	aattgctaag	13920
gaaatcgag	atcttatgat	ggaatcccca	ggaaagaatc	ctgaggagat	tttaaaagag	13980
aagccagagc	tgcttcccat	gtcagatgaa	ggggaattgc	agaaaattat	cgcagaggtg	14040
gttcttgcaa	atcctgaatc	tatcgtagac	tataaaaaatg	gaaagactaa	ggctctagga	14100
ttcctagtcg	ggcagattat	gaagcgtaca	gcaggaaaaag	ctcctcccaa	gcgagtgaac	14160
gaacttttac	ttttagaatt	agataagggc	tagaattttc	tgtcacagtc	tgtcttaaaa	14220
aatcataaaa	gcatgttaga	gatctttcta	acatgctttt	tttatctaaa	tacacatttc	14280
taagtgtcaa	aaacgaaagc	agaaaatttc	gatttgcctt	tctacctaca	ctttatggat	14340
ccatcagaat	taaattttgc	aaagccatgt	ctacgcggga	gataattctt	tttaagtgtac	14400
aagaaaattct	tgtgctcggc	ttgctttctt	attcttattg	acgtattgct	tgtatcagata	14460
ttcattttga	tttaggtact	aaaatgcgat	tttcgctctg	cggatttccct	ctagtttttt	14520
cttttacatt	gctctcagtc	ttcgacactt	ctttgagtgc	tactacgatt	tctttaacctc	14580
cagaagatag	ttttcatgga	gatagtcaga	atgcagaacg	ttcttataat	gttcaagctg	14640

gggatgtcta	tagccttact	ggtgatgtct	caatatctaa	cgctcgataac	tctgcattaa	14700
ataaagcctg	cttcnatgtg	acctcaggaa	gtgtgacgtt	cgcaggaaat	catcatgggt	14760
natattttaa	taatatctcc	tcaggaaacta	caaaggaagg	ngctgtactt	tggtgccaag	14820
atcctcaagc	aacggcacgt	ttttctgggt	tctccacgct	ctcttttaat	cagagccccg	14880
gagatattaa	agaacaggga	tgtctctatt	caaaaaatgc	acttatgtct	ttaaacaatt	14940
atgtagtgcg	ttttgaacaa	aaccaaagta	agactaaagg	cggagctatt	agtggggcga	15000
atgttactat	agtaggcaac	tacgattccg	tctctttcta	tcagaatgca	gccacttttg	15060
gaggtgctat	ccattcttca	ggccccctac	agattgcagt	aaatcaggca	gagataagat	15120
ttgcacaaaa	tactgccaaag	aatgggttctg	gaggggcttt	gtactccgat	ggtgatattg	15180
atattgatca	gaatgcttat	gttctatttc	gagaaaatga	ggcattgact	actgctatag	15240
gtaagggagg	ggctgtctgt	tgtcttccca	cttcaggaaag	tagtactcca	gttctctattg	15300
tgactttctc	tgacaataaa	cagttagtct	ttgaaagaaa	ccattccata	atgggtggcg	15360
gagccattta	tgctaggaaa	cttagcatct	cttcaggagg	tcctactcta	tttatcaata	15420
atatacata	tgcaaattcg	caaaatttag	gtggagctat	tgccattgat	actggagggg	15480
agatcagttt	atcagcagag	aaaggaacaa	ttacattcca	aggaaaccgg	acgagcttac	15540
cgtttttgaa	tggcatccat	cttttataaa	atgctaaatt	cctgaaatta	caggcgagaa	15600
atggatactc	tatagaattt	tatgatacta	ttacttctga	agcagatggg	tctaccacaa	15660
tgaatatcaa	cggagatcct	aaaaataaag	agtacacagg	gaccatactc	ttttctggag	15720
aaaagagtct	agcaaacgat	cctagggatt	ttaaatctac	aatccctcag	aacgtcaacc	15780
tgtctgcagg	atacttagtt	attaaagagg	gggccgaagt	cacagtttca	aaattcacgc	15840
agtctccagg	atcgatttta	gttttagatt	taggaaccaa	actgatagcc	tctaaggaag	15900
acattgccat	cacaggcctc	gcgatagata	tagatagctt	aagctcatcc	tcaacagcag	15960
ctgttattaa	agcaaacacc	gcaataaaac	agatatccgt	gacggactct	atagaactta	16020
tctcgctac	tggcaatgcc	tatgaagatc	tcagaatgag	aaattcacag	acgttccctc	16080
tgctctcttt	agagcctgga	gccgggggta	gtgtgactgt	aactgctgga	gatttccctac	16140
cggtaagtcc	ccattatggt	tttcaaggca	attggaaatt	agcttggaca	ggaactggaa	16200
acaaagtggg	agaattcttc	tgggataaaa	taaattataa	gcctagacct	gaaaaagaag	16260
gaaatttagt	tcctaataatc	ttgtggggga	atgctgtaga	tgtcagatcc	ttaatgcagg	16320
ttcaagagac	ccatgcatcg	agcttacaga	cagatcgagg	gctgtggatc	gatggaattg	16380
ggaatctctt	ccatgtatct	gcctccgaag	acaatataag	gtaccgctcat	aacagcgggtg	16440
gatatgttct	atctgtaaat	aatgagatca	cacctaaaga	ctatacttcg	atggcatttt	16500
cccaactctt	tagtagagac	aaggactatg	cggtttccaa	caacgaatac	agaatgtatt	16560
taggatcgta	tctctatcaa	tatacaacct	ccctagggaa	tattttccgt	tatgcttcgc	16620
gtaaccctaa	tgtaaacgtc	gggattctct	caagaagggt	tcttcaaaat	cctcttatga	16680
tttttcattt	tttgtgtgct	tatggtcatg	ccaccaatga	tatgaaaaca	gactacgcaa	16740
atttccctat	ggtgaaaaac	agctggagaa	acaattggtg	ggctatagag	tgcggaggga	16800
gcatgcctct	attggtattt	gagaacggaa	gacttttcca	aggtgccatc	ccatttatga	16860
aactacaatt	agtttatgct	tatcagggag	atttcaaaga	gacgactgca	gatggccgta	16920
gatttagtaa	tgggagttaa	acatcgattt	ctgtacctct	aggcatacgc	tttgagaagc	16980
tggcactttc	tcaggatgta	ctctatgact	ttagtttctc	ctatattcct	gatattttcc	17040
gtaaggatcc	ctcatgtgaa	gctgctctgg	tgattagcgg	agactcttgg	cttgttccgg	17100
cagcacacgt	atcaagacat	gctttttag	ggagtggaaac	gggtcgggtat	cactttaacg	17160
actatactga	gctcttatgt	cgaggaaagta	tagaatgccg	cccccatgct	aggaattata	17220
atataaactg	tggaaagcaa	tttcgttttt	agaagggttc	cattgcctgt	gtggttccgg	17280
atcttaacta	taaatcctgg	actatggatc	ataggcattg	ggtctctcga	acttgtgtgg	17340
agaataacga	cattttatat	gcataacgga	atactcgat	cacctcagcc	cctagagaca	17400
ttcttttaggg	gttctttatt	tgtctaaact	tcgtatttta	tcgagaatcc	tttacgttct	17460
tggtttgctt	gtctccgagg	agttctctaa	cgaatcatag	ggattccagg	gttctgttcc	17520
ttgagtcctt	tggcagctga	tttgcgtctt	tctcaggagt	agagcgtgtg	gtttcagggc	17580
ttgggactcc	tagtaagacg	agccattctg	atagcctctc	taggagagcg	cttcgaagag	17640
gttctctgaa	ctgcttctaa	gtaaaaattt	aaagagaagt	ctagtttttt	cgatacattg	17700
acttcttttt	tgaaccaga	cactcattgc	tagccgaatt	ttaagagttc	atgagcatga	17760
ttctctgtaa	atcctcgcaa	tgagcttttt	gtcttctcac	cttatgatgt	gctttctata	17820
agtattttaaa	tgaactttta	ttaaaagagt	tttcgctata	acctttcgct	cattttttcc	17880
tttcttgctg	tgataccgct	aactgatagc	actacaagct	ctctttcaac	gtctctctta	17940
gatgaaggaa	accacacaatc	catgaggaaa	cttcgtattc	ttgcgatcgt	tctcatagct	18000
ttgagcatta	ttttgattgc	aggtggtgtg	gtattgctta	ctgtagcgat	ccctggatta	18060
agttcagtc	tttcttcccc	ggcagggatg	ggtgcctgtg	ctttgggatg	tgtgatgctt	18120
gcttttagga	tcgatgttct	tctgaagaaa	cgagaagtcc	ctatagtctt	cgcactctga	18180
actacgacac	caggaactgg	cagccctaga	agtggtattt	ctatttcagg	agctgatagc	18240
accatacgtt	ctcttcctac	gtatctcttg	gacgagggac	atccacaatc	catgaggaaa	18300
cttcgtattc	ttgcgatcgt	tctcatagtt	tttagcatta	ttttgattgc	aagtgggtgtg	18360
gtattgctta	ctgtagcgt	ccctggatta	agttcagtc	tttcttcccc	ggcagggatg	18420
ggtgcctgtg	ctttgggatg	tgtgatgctt	gcttttagga	tcgatgttct	tctgaagaaa	18480

cgagaagtcc	ctatagttct	cgcatctgta	actacgacac	caggaactgg	cagccctaga	18540
agtggtat	ctatttcagg	agctgatagc	accatacgtt	ctcttcctac	gtatcccttg	18600
gacgagggac	atccacaatc	catgaggaaa	cttcgtat	ttgcatcgt	tctcatagtt	18660
tttagcatta	ttttgattgc	aagtgggtg	gtattgctta	ctgtagcgat	ccctggatta	18720
agctcgatca	tttcttcccc	agcggagatg	ggtgcttgtg	ctttgggatg	tgtgatgctt	18780
gctttgggga	tcgacgttct	tctgaagaaa	cgagaagtcc	ctatagtagt	tcccgcacct	18840
attcctgaag	aagtcgtcat	agatgatata	gatgaagaga	gtatacggct	gcagcaggaa	18900
gctgaagccg	cttttagcaag	acttcctgag	gagatgagtg	catttgaagg	ttacataaaa	18960
gttgctgaga	gtcattttgga	gaacatgaaa	agcctgcctt	atgatgggtca	tgggctagaa	19020
gagaaaaacga	aacatcagat	aagagtcgtc	agatcttctt	tgaaggctat	ggttccagaa	19080
tttttagata	tcagaagaat	ttttgaagaa	gaagagttct	ttttctcttc	agctcgcaaa	19140
cgacttatag	atttagctac	tactttagta	gagagaaaaa	ttttaacaga	gcaacttgag	19200
cgcaataatt	taaggaaagc	gttttcttat	ttatatcagg	actcaatttt	taaaaaaatt	19260
attgataact	tcgagaagtt	agcatggaaa	tttatgattt	tgagtaaata	aatttgtcga	19320
tttacaatta	tttttgaaaa	tcatgaacat	ggtgtagcaa	agagcctgtt	acacaagaat	19380
gcagtgttac	tggagaaggt	aatctatagg	agtttgcaaa	aaagctatag	agatataggc	19440
atgtcatctg	caaagatgaa	aatcttgac	ggcaaccctt	ttttctcttt	ggaagataat	19500
aaaaagaca	taatgaaaga	acacgcagag	agcttgaaa	gtctcagtag	ctataggaa	19560
gtatttttag	ctctatctga	tgagaacgtt	gtagatacac	ctagcgatcc	aaagaaatgg	19620
gatttgtcag	gaatcccctg	tagggacgag	ttgtctgaga	tttctcgtga	tgaacagtgg	19680
cagaagaaag	cacatctaaa	gcatacaag	tccctctata	cgcaagctag	ggatcgttta	19740
acagaccaga	gctctaaaga	aaatcagaaa	gagttagaga	aagctgaaca	agagtacata	19800
tcttcttggg	aacgggttaa	aaaatttgag	attgagagag	tacaggagag	gatacaggca	19860
attcaaaagc	tttatcctaa	tatcctcgag	agagaagaag	aaaccacagg	tcaggagact	19920
gtgactccaa	ctgttcaagg	gacgacgct	tcatacagatt	taacagatat	tttaggaaga	19980
atagaggtct	ccagtaggga	ggataatcag	aatcaagagt	cttgtgtaaa	agtcttaaga	20040
agtcatgagg	tagaaatgag	ctgggaagtc	aaacaagagt	atggccctaa	gaaaaaagaa	20100
tttcaggatc	aaatgggttc	tttagagagg	ttttttacag	agcatattga	agagttagaa	20160
gtattacaga	aggactactc	taaacacttg	tcttatttta	aaaaagtaaa	caataagaaa	20220
gaggttcaat	atgcgaagtt	taggttgaag	gttttagagt	cagattttaga	agggattcta	20280
gctcagactg	agagtgtcga	gagtctgtta	actcaagaag	aacttcgat	tcttgcaact	20340
cgggtagcct	tagagaaagc	gtttttcaaa	ggagtgctat	gttgccgct	agcaagcaaa	20400
gcaaaaccct	attttgaaaga	ggatcccaga	ttccaagatt	ctgatacgca	attgcgagct	20460
ctgactctaa	ggttacagga	ggctaaggca	agcctggaag	aagagataaa	gagattttca	20520
aatcttgaga	acgatattgc	agaggaaaga	cgccttctta	aagagagcaa	gcagacgttc	20580
gaaagagcag	gttttaggggt	tctccgagaa	attgcagtcg	agtcacttta	tgatttgcgt	20640
tccttaacaa	atacatggga	agggacccca	gagagtgaga	aggtctattt	tagcatgtat	20700
cttaattatt	acaacgaaga	gaaacgtagg	gmnaaaacaa	gattggttga	aatgacacag	20760
aggtatgact	attttaaaat	ggccttgga	ggtatgcagt	ttaattgaaga	agcccttttg	20820
caagaggaac	tctctattca	agctcccagt	gaataacaag	aatccgaggc	aagagctcgg	20880
catgtcgtc	gctataggct	acgagttgcc	caatctcggt	tggctgattt	agaagctgga	20940
gtcatccaga	aacgtaaaac	aatcaaaagat	ttgttcaaga	aacgacagtc	tcaaccttct	21000
tctaagaaat	agaaaatttc	gtccatgctt	ccagggtttt	gaaatgagaa	aaagaccttg	21060
gaataaaaata	attgatatga	gtagcttagt	tgcttttaact	tatgtttttg	agcatgatga	21120
catcacagat	tcataatgca	agtattctta	tctctcaac	tacccccccc	cccccgacg	21180
ctctctaggg	gtttcttgggt	ctaaacttcg	tagttttatc	atcactcttt	tagttcttgg	21240
tgtgcttttg	ttgaccttgg	ggattccggg	actcactgca	gggatctctt	ttggagccgg	21300
tttgggattt	tctgcttttag	gaggagtgtc	cgtgatttcg	ggacttctat	tccttctagt	21360
aagacgagag	gttccgacag	tacgttcaga	ggaaattccc	agaggggttt	ctgtgacccc	21420
ttctgaagag	cctgctctag	agaaggctca	aaaagaaccg	gagacaaaga	aaatttttaga	21480
tcggttgccg	aaggaattgg	atcagttaga	tacgtatatt	caggaagtgt	ttgcattgtt	21540
agagaggtcg	aaggatccta	agtacgaaga	tcgaggtctt	ttaacagagg	cgaaggagaa	21600
acttcagatt	tttgacgttg	ttgagaaaga	tatgatgtca	gagtttttag	acatacaacg	21660
agtgttgaat	gaggaagcat	attatgtaga	acattgtcaa	gatccccctag	agaatatagc	21720
ctacgagatt	ttctcttccc	aagagcttcg	tgactactac	tgtgcagggg	tgtgtgggta	21780
tttgccttct	gggtagctc	gagcggatcg	attaaagaga	tcagttaaag	aggtaattgga	21840
tcgcttttat	aggggtgacct	ggaaatcttg	ggaggcatca	gtcatgttgg	atcatagcta	21900
tggggtagcg	cgagagttat	tcaagaaggc	agtaggagta	ctagaggaga	gtgtctataa	21960
aattctgttt	aagagctata	gagatgcgtt	ttatgaatgt	gagaaggcaa	agatccagag	22020
ggatgggctg	ttcaaatggt	tataggatac	gagtgctcat	gcggaacaaa	ggttttaggga	22080
tatcaatggt	tgttgggagg	acttaaagca	aacgatcttt	tgggtaggag	aacatgattg	22140
tacggacata	gagaccgtac	gtaaaagctg	tatgtggctg	gatcgttatg	cagataaatt	22200
tattttgagg	gaaaaagagg	aaaagatgga	gcgtcatgag	ctctttcatg	cgactatggt	22260
ccgaaaagca	tctgggcacg	cgtatgctaa	agctaaagca	gcctttgaaa	aggagagatc	22320

taätgagaat	cagaggaag	tcaaggatgt	tgaaaaatgg	ttatctaaag	gtttagcgga	22380
gtttcgtaat	caagagtctc	gcagagctcg	ggagaggctg	agagagctgc	aaactttgta	22440
tcctgaggtt	tctgtagaag	agagagtgtt	agagagacaa	aggactaaaa	aagttaatct	22500
ggagaacttg	tatgcagata	tagaaaagaa	gtatcaccac	tgtgttcgag	agcaagagca	22560
ttactggaaa	gaggttagaga	acaaggaagc	agagtatagg	gagaacggag	aaaaggttct	22620
ctctgccgag	gaggtgtcag	agtgtcttca	gaggttggaa	gattgttttag	agacgtgggtc	22680
taagaaatta	acaaaagcgg	aagagagtgt	ctttgagatg	aagtttgatg	cgacagaaaa	22740
actagggaat	aaagtacttt	ctgatgtaac	gaaccgtctt	gagattttat	gtgaagatgc	22800
tgaggagatg	atttttcgaa	tcgaagagat	agagatgact	ctgcgtatgg	tagagcttcc	22860
actacttttt	atgaaaaata	cttttgagaa	agcctctcta	caatacaaca	gctgcaaaaga	22920
gatgtttagcc	aaagttagagc	cccaatgtaa	ggaaägccca	acctatagaa	gtagccaaga	22980
gcgcttagaa	aggttgaatc	aggatttaca	aacagcatat	acaaattgcc	aggagagact	23040
ccagggtttt	tcagatttgg	aatcaaaagt	acgtacatgt	agagatcatc	ttagagagca	23100
gatgaaacat	ttcgaagttc	aaggactgaa	ttttataaac	gaagagcttt	tatgggtcgg	23160
ggcagagctc	tttacacaag	ccagattgga	tctagtagca	acagttccgt	atatggagtt	23220
ctatttgcag	taccataata	ttaaaagaga	aaaagttcga	tcccaatgga	tggcgaagac	23280
cgagaggtat	agagagattc	ggcaggcatt	tcaagggtg	atgaaggaa	atttgttagc	23340
agaagatacg	atcttgaaag	aagaagatta	ttggctgctt	cgcatgatt	ggttgcgtcg	23400
tgatgagagg	aagaatagac	aaagacgttt	aatctgtaat	aagatagcag	cagcgcaaca	23460
gcgagtcaaa	ggcttctaac	ctgaagagat	ttaaaagatc	ctgaaagaga	aaacacctct	23520
tgtggctaga	gtgcgttctt	tatttactcg	cgaggaccat	acctagcata	aaactccagg	23580
agctgtgttt	ctttaaaatt	ctttgaataa	aatactatat	attagtagct	tagtgggttt	23640
aattttatgtg	tttgatcgcg	atggcaccac	agattcataa	tgcaagtact	tctatctcgg	23700
cagctacccc	ccccccaac	actctgtagg	gtcgtattct	tctccatcta	aacttcgctg	23760
tttagcgatt	acttttttag	tttttggtat	gctcttactg	atttcaggag	ctctctttct	23820
gacgttaggg	attccaggat	tgagtgcagc	aatttctttt	ggattaggca	tcggtctctc	23880
cgcattagga	ggagtgtcga	tgatttcggg	actactatgt	cttttagtaa	aacgagagat	23940
tccgacagta	cgaccagaag	aaattcctga	aggggtttcg	ctggctcctt	ctgaggagcc	24000
agctctacag	gcagctcaga	agactttagc	tcagctgcct	aaggaattgg	atcagttaga	24060
tacagatatt	caggaagtgt	tcgcatgttt	aagaaagctg	aaagattcta	agtatgaaag	24120
tcgaagtttt	ttaaacgatg	ctaagaagga	gcttcgagtt	tttgactttg	tgtttgagga	24180
tacctctcg	gagattttcg	agttgcggca	gatttgtggt	caagagggat	gggatttaaa	24240
ctttttgatc	aatgggggac	gaagcctcat	gatgactgca	gaatctgaat	cgcttgattt	24300
gtttcatgta	tcgaagcggc	tagggatatt	accttctggg	gatgttcgag	gggaggggtt	24360
aaagaaatct	gcgaaggaga	tagtcgctcg	tttgatgagc	ttgcattgcg	agattcacaa	24420
ggtggcggtg	gcgtttgata	ggaattccta	tgcatgggca	gaaaaggcgt	ttgcgaaagc	24480
gttgggagct	ttagaagaga	gtgtgtatcg	gagctcgacg	cagagttata	gagataaatt	24540
tttagagagt	tagagggcga	agatcccattg	gaatgggcat	ataacctggg	taagagatga	24600
tgcaagagtg	gggtgtgctg	aaaagaagct	tcgggatgcc	gaggaacggt	ggaagaaatt	24660
taggaaagca	gtcttttggg	tagaagaaga	cgggggcttt	gacatcaata	atctccttgg	24720
agactggggg	acagtgcctg	atccttatag	acaagagaga	atggacgaga	taacgttcca	24780
tgagttgtat	gaaaaaacta	cgtttttgaa	aagactgcac	agaaagtgtg	cgtttagcgaa	24840
aacaaccttt	gaaaagaaga	gatctaaaaa	gaatttgacg	gcagtcgagg	aggcgaatgc	24900
acgttaggtg	aaatatgtaa	gggatgtgta	tgatcaggag	tttcagaaag	caggggagag	24960
attagagaaa	ctgcatgctt	tgtatcctga	ggtttcagtc	tctataagag	agaacaaaat	25020
acaagagacg	cgctctaatt	tagagaaagc	ctatgaggct	atcgaagaga	actatcgttg	25080
ctgtgtccga	gagcaagagg	actactggaa	agaagaagag	aaaagggaag	cggagttagg	25140
ggagagggga	aacaagattc	tttctcctga	ggagctggaa	agttcttttg	agcaattcga	25200
ccatggtttg	aaaaattttt	ctgagaaatt	aatggaattg	gaagggcata	tcttaaaact	25260
tcagaaagaa	gccacagcag	aggtggagaa	taaaatactt	tcagatgcag	agagccgcct	25320
tgagattgta	tttgaagatg	tcaaggagat	gccctgtcga	attgaggaga	tagagaagac	25380
gctgcgtatg	gcggagctgc	ccctacttcc	tacgaagaag	gcgtttgaga	aggcctgctc	25440
acaatataat	agctgcgcag	agatgttgga	gaaggtgaag	ccttactgca	aggagagcct	25500
cgcttatgtg	actagcaaag	agcgtttagt	gagcttggat	gaagatttac	gacgagccta	25560
cacagagtgt	cagaagagat	tccaggggga	ttcgggtttg	gagtcggaag	taagagcctg	25620
tcgagagcaa	ctgcgagagc	ggatccaaga	gtttgaaact	caagggctgg	acttgggtgga	25680
aaaagagttg	ctttgtgtga	gtagtagatt	aagaaatata	gagtgcgatt	gtgtatctgg	25740
tgtaaagaaa	gaagcacctc	ctggtaagaa	gttttatgcc	cagtattatg	atgagattta	25800
tcgagttaga	gttcaatccc	gatggatgac	gatgtctgag	agattgagag	agggagtcca	25860
agcatgcaac	aagatgttga	aggcaggcct	aagcgaagaa	gataaggttc	ttaaagaaga	25920
agagtatttg	ttgtatcgag	aggagagaaa	gaataaagag	aaacgttttg	ttggtactaa	25980
gatagtagca	acgcagcagc	gagttgcagc	atttgaatcc	atagaagttc	ctgagattcc	26040
tgaggcccca	gaggagaaac	cgagtttgct	ggataaagcg	cgttctttat	ttactcgcga	26100
ggaccatttc	tagaactatt	ctaggagtct	atgtgcacta	ttttttaaga	ggtttattat	26160

tccgtgggta	tgtctgagag	actttgatta	aatgggatat	tattatatcc	tagttgctct	26220
aatcaatatt	cctcttatga	ttttgggtatt	cgatcatgac	tgcagcacca	gctattctac	26280
acgtatcccc	gacgccccct	gaagaaacaa	aattcgttat	tcctaaagat	agtaaactctc	26340
gcgctcttgg	gattacttta	ttagtcgtag	gcacccctct	ggtagtttgt	ggtgcgattg	26400
tactcagtg	agtgatttct	ggattgagtg	cactcattgt	ttgtggattg	ggtattagta	26460
cgatttctct	aggagtgtgc	ctatttgttt	taggattgat	attattactt	agaaagcggg	26520
aacttacctt	agaacagatc	gaggctaagc	aaattgcgga	gacctttgct	gatgaactga	26580
aagaactaga	aatgtacatt	cagtcgacag	agaaaagcct	agagaagata	gaagggtccc	26640
gttatagtga	ccaagggttt	ctgaatcgtg	ccacccaaaa	aatcttagat	ttagaatctt	26700
cattgagctc	tattacttct	gagtttcgtg	atcttaggca	actctttgat	gaagaaaaaa	26760
tagagttact	ttctggagaa	aggcttttag	aatttattgc	agcgaattta	tttaaacaa	26820
gaagagatgt	ctattttaa	ttagggaatt	tagcagacat	tcgtgcgtac	atggggccca	26880
acaattataa	agttgctgat	gtcatagaaa	aagctaaagc	agttgtgcat	gagtttatag	26940
ttctgactac	aatggctagg	gaattagagt	tttttttcta	aaaaataaat	atgggtttatt	27000
aaaggggatg	taccaggaga	atctaagatt	gttggaagg	cttctttata	atagtgttca	27060
aaagagctat	gcggtacggc	tgttttccta	tgaaaagaca	aagatgggtc	acgatactcc	27120
gctgattcct	tggaagagg	ataaggaaaa	gctgagaaag	cttctttaga	cttctttaga	27180
gcaacagaag	attctcctag	attatggaaa	atctatcttt	tggctgaatg	agaacgatga	27240
gatcaattta	aacgatcctt	ggagtgggg	tccttaatac	gtgaggacta	ggaaagtatt	27300
ccaagagggt	gacgacagtg	aacgttgga	tcataaggta	ctcattcaca	aactcgagga	27360
cgattatgag	aaacttctag	aggaaagtcc	aaaagagtct	actgaagcaa	ataagaagct	27420
tttatctgac	ttagtagatc	gtcttgaaga	tgctaagaca	aaatttttcc	tgaagaaaca	27480
ggaggagggtg	gagactcgcg	ttaaggatct	tagagctcga	tatggaggca	cagtagatcc	27540
taagcaggat	acggaagcta	agaagaaagt	cgaattggag	gctagcttag	aaaccttttt	27600
agattccatc	gaatcagagc	tagtacagtg	tttagaagat	caagatatat	attggaaaga	27660
acaggatgtc	aaagatctag	cacgtacgca	agagctcgag	gaacaagata	ttgaagcgaa	27720
gagggaagaa	gctgccgaag	acctaagaaa	gtcttaata	gcgtttaaag	aagtcaaaaa	27780
ctatgttaga	tagggctaaa	tggtcatatt	aaaatgctga	ggacagtatt	acctgggtgga	27840
ctagtcagat	agaaatgaag	gatatgaaag	caagactgaa	gatcttaaaa	gaagatataa	27900
caagtgttct	acctgaaata	gatgagattg	aaactgtgtt	aagcttagag	gagcttctct	27960
tgcttacgac	cagggaaactc	ttaactaagt	cctacttaaa	gtttaagatt	tgctcgga	28020
cactattaaa	aatgacttct	gtgtttgaga	acaatatcta	tgctcaggag	tacgaggttc	28080
agctgcaaaa	tctagggttt	aagttacaag	gtatatctca	gagattcgga	aagaaacaag	28140
acgattttgc	gaatctagag	gaacaggttg	ctttgcaaaa	gaaacgactc	agagagctca	28200
ctcagaattt	tgaaatacaa	ggattcaatt	tcataagaa	agattttaag	gcagccgcta	28260
aagatcttta	tataagaagt	acagctgaac	aaaagatgaa	ctttgatgtg	ccttgcatgg	28320
agctcttccg	taggtatcat	gaggaggtca	acaagccgct	tcttgagttg	atgtacaatt	28380
gtgcagacag	ttatagagat	gctaagaaaa	agctttgtct	tctacgtctt	gatgaaaaag	28440
agttattaca	aaaagaaatc	aagaaagagg	aattttatca	aaagaaacaa	caaaggcatg	28500
cagatagatc	acgtcactac	aggtatcaaa	agctacgaat	tgctgaagag	cttgctcttg	28560
agctgaagaa	gaaatctaa	tcactaaagc	ctagtttaag	gttcttttga	attgggccct	28620
gtgtttccat	ttctctaggg	atcctcttag	ctgaggatct	tctttgtacc	tcttttgatt	28680
cgaaaagagg	tgctattgtg	agttgccaat	agcaacgatc	caccttcggt	tttgaagaa	28740
tacatcagtt	gctaagggaa	cttttcagaa	aatatacata	aaaactccca	agattttggc	28800
ttggaaagcg	agcctttctt	gctacttttg	ttatacaaaa	agtgttctat	tttaacgtgc	28860
gtatcatttg	tgactaagag	atagacttgc	tttctttatc	taatcttctg	tattggaaag	28920
aaagccccct	gagggaaaaa	aaggttggtt	tgaagattcc	actccgcttt	ttattgatat	28980
cattagtacc	tacgctttct	atgtcgaatt	tattaggagc	tgctactacc	gaagagttat	29040
cggctagcaa	tagcttcgat	ggaactacat	caacaacaag	cttttctagt	aaaacatcat	29100
cggctacaga	tgccaccaat	tatgttttta	aagattctgt	agttatagaa	aatgtaccca	29160
aaacagggga	aactcagctc	actagtgtgt	ttaaaaatga	cgctgcagct	ggagatctaa	29220
atttcttagg	aggggggattt	tctttcacat	ttagcaatat	cgatgcaacc	acggcttctg	29280
gagctgctat	tggaagtga	gcagctaata	agacagtcac	gttatcagga	ttttcggcac	29340
tttcttttct	taaatcccca	gcaagtacag	tgactaatgg	attgggagct	atcaatgtta	29400
aaggggaattt	aagcctattg	gataatgata	aggtattgat	tcaggacaat	ttctcaacag	29460
gagatggcgg	acaattaatt	gtgcaggctc	cttgaagatc	gcaaacaata	agtccttttc	29520
ttttatttga	aatagttctt	caacacgtgg	cggagcgatt	cataccaaaa	acctcacact	29580
atcttctggt	ggggaaactc	tatttcaggg	gaatacagcg	cctacggctg	ctggtaagg	29640
aggtgctatc	gcgattgcag	actctggcac	cctatccatt	tctggagaca	gtggcgacat	29700
tatcttttga	ggcaatacga	taggagctac	aggaaccgtc	tctcatagtg	ctattgattt	29760
aggaactagc	gctaagataa	ctgcgttacg	tgctgcgcaa	ggacatacga	tatactttta	29820
tgatccgatt	actgtaacag	gatcgacatc	tggtgctgat	gctctcaata	ttaatagccc	29880
tgatactgga	gataacaaag	agtatacggg	aaccatagtc	ttttctggag	agaagctcac	29940
ggaggcgaga	gctaaagatg	agaagaaccg	cacttctaaa	ttacttcaaa	atgttgcttt	30000

taaaaatggg	actgtagttt	tgaaaagggtg	atgtcgtttt	aagtgcgaac	ggtttctctc	30060
aggatgcaaa	ctctaagttg	attatggatt	tagggacgtc	gttggttgca	aacaccgaaa	30120
gtatcgagtt	aacgaatttg	gaaattaata	tagactctct	caggaaacggg	aaaaagataa	30180
aactcagtg	tgccacagct	cagaaagata	ttcgtataga	tcgtcctgtt	gtactggcaa	30240
ttagcgatga	gagtttttat	caaaatggct	ttttgaatga	ggaccattcc	tatgatggga	30300
ttcttgagtt	agatgctggg	aaagacatcg	tgatttctgc	agattctcgc	agtatagatg	30360
ctgtacaatc	tccgtatggc	tatcagggaa	agtggacgat	caattgggtct	actgatgata	30420
agaaagctac	ggtttcttgg	gcgaagcaga	gttttaatcc	cactgctgag	caggaggctc	30480
cgtagattcc	taatcttctt	tggtgttctt	ttatagatgt	tcgttccttc	cagaatttta	30540
tagagctagg	tactgaaggt	gctccttacg	aaaagagatt	ttgggttgca	ggcatttcca	30600
atgttttgca	taggagcgg	cgtgaaaatc	aaaggaaatt	ccgtcatgtg	agtggagggtg	30660
ctgtagtagg	tgctagcacg	aggatgccgg	gtggtgatac	cttgtctctg	ggttttgctc	30720
agctctttgc	gcgtgacaaa	gactacttta	tgaataccaa	tttcgcaaag	acctacgcag	30780
gatctttacg	tttgacgac	gatgcttccc	tatactctgt	ggtagtatc	cttttaggag	30840
agggaggact	ccgcgagatc	ctgttgctt	atgtttccaa	gactctgccg	tgctctttct	30900
atgggcagct	tagctacggc	catacggatc	atcgcatgaa	gaccgagtct	ctaccccccc	30960
cccccccgac	gctctcgacg	gatcatactt	cttggggagg	atatgtctgg	gctggagagc	31020
tggaactcg	agttgctgtt	gaaaatacca	gcggcagagg	atttttccaa	gagtacactc	31080
catttgtaaa	agtcgaagct	gtttacgctc	gccaaagatag	ctttgtagaa	ctaggagcta	31140
tcagtcgtga	tttttagtgat	tcgcactctt	ataaccttgc	gattcctctt	ggaatcaagt	31200
tagagaaacg	gtttgcagag	caatattatc	atgttgtagc	gatgtattct	ccagatgttt	31260
gtcgtagtaa	ccccaaatgt	acgactaccc	tactttccaa	ccaagggagt	tggaagacca	31320
aaggttcgaa	cttagcaaga	caggctggta	ttgttcaggc	ctcaggtttt	cgatctttgg	31380
gagctgcagc	agagcttttc	gggaactttg	gcttttaagt	gcggggatct	tctcgtagct	31440
ataatgtaga	tgccggtagc	aaaatcaaat	tttagcgatt	tctcttccga	tgctattttt	31500
ccatggctat	ttttaaaatg	atagccatgg	ttatagatac	gtagtcctta	tttcaaagaa	31560
gacactgttg	cattagatac	gctctctgat	ccctcaaaat	cacattttgg	tatctgattg	31620
ctaagattgc	aggataccac	gcatcttaag	agaaaggcgc	tcttacctag	tagagggtga	31680
gtgaatttct	tgacttggtt	ctcctattgg	tgtatctctt	aaaatattaa	attcaaaatc	31740
aaagtataata	ttttacaatg	aagtccttct	tcccgaagt	tgtattttct	acatttgcta	31800
ttttcccttt	gtctatgatt	gctaccgaga	cagtttttga	ttcaagtgcg	agtttcgatg	31860
ggaataaaaa	tggttaatttt	tcagttcgtg	agagtcagga	agatgctgga	actacctacc	31920
tattttaagg	aaatgtcact	ctagaaaata	ttcctggaac	aggcacagca	atcacaaaaa	31980
gctgttttaa	caacactaag	ggcgatttga	ctttcacagg	taacgggaac	tctctattgt	32040
tccaaacggg	ggatgcaggg	actgtagcag	gggctgctgt	taacagcagc	gtggtagata	32100
aatctaccac	gtttataggg	ttttcttcgc	tatcttttat	tgctctcct	ggaagttcga	32160
taactaccgg	caaaggagcc	gttagctgct	ctacgggtag	cttgagtttg	acaaaaatgt	32220
cagtttgctt	ttcagcaaaa	acttttcaac	ggataatggc	ggtgctatca	ccgcaaaaac	32280
tctttcatta	acagggacta	caatgtcagc	tctgttttct	gaaaatacct	cctcaaagaa	32340
aggcggagcc	attcagactt	ccgatgccct	taccattact	ggaaaccaag	gggaagtctc	32400
tttttctgac	aatacttctt	cggattctgg	agctgcaatt	tttacagaag	cctcgggtgac	32460
tatttctaata	aatgctaaag	tttcttttat	tgacaataag	gtcacaggag	cgagctcctc	32520
aacaacgggg	gatatgtcag	gaggtgctat	ctgtgcttat	aaaactagta	cagatactaa	32580
ggtcaccctc	actggaaatc	agatgttact	cttcagcaac	aatacatcga	caacagcggg	32640
aggagctatc	tatgtgaaaa	agctcgaaat	ggcttcggga	ggacttaccc	tattcagtag	32700
aaatagtgtc	aatggaggta	cagctcctaa	agggtggagcc	atagctatcg	aagatagtgg	32760
ggaattgagt	ttatccgccg	atagtgggtga	cattgtcttt	ttagggaata	cagtcacttc	32820
tactactcct	gggacgaata	gaagtagtat	cgacttagga	acgagtgcga	agatgacagc	32880
tttgcggtct	gctgctggta	gagccatcta	cttctatgat	cccataacta	caggatcatc	32940
cacaacagtt	acagatgtct	taaaagttaa	tgagactccg	gcagattctg	cactacaata	33000
tacagggaac	atcatcttca	caggagaaaa	gttatcagag	acagaggccg	cagattctaa	33060
aaatcttact	tcgaagctac	tacagcctgt	aactctttca	ggagggtactc	tatctttaaa	33120
acatggagtg	actctgcaga	ctcaggcatt	cactcaacag	gcagattctc	gtctcgaaat	33180
ggacgttaga	actactctag	aacctgctga	tactagcacc	ataaacaatt	tggtcattaa	33240
catcagttct	atagacgggtg	caaagaaggg	aaaaatagaa	accaaagcta	cgtcaaaaaa	33300
tctgacttta	tctggaacca	tcactttatt	ggacccgacg	ggcacgtttt	atgaaaatca	33360
tagtttaaga	aatcctcagt	cctacgcacat	cttagagctc	aaagcttctg	gaactgtaac	33420
aagcaccgca	gtgactccag	atcctataat	gggtgagaaa	ttccattacg	gctatcaggg	33480
aacttggggc	ccaattgttt	gggggacagg	ggcttctacg	actgcaacct	tcaactggac	33540
taaaactggc	tatatctcta	atcccgagcg	tatcggctct	ttagtcccta	atagcttatg	33600
gaatgcattt	atagatatta	gctctctcca	ttatcttatg	gagactgcaa	acgaagggtt	33660
gcaggggagac	cgtgcttttt	ggtgtgctgg	attatctaac	ttcttccata	aggatagtag	33720
aaaaaacacga	cgcggttttc	gccatttgag	tgccggttat	gtcataggag	gaaacctaca	33780
tacttggttca	gataagattc	ttagtgtctg	attttgtcag	ctctttggaa	gagatagaga	33840

ctacttttga	gctaagaatc	aaaggtacag	tctacggagg	aactctctat	taccagcaca	33900
acgaaacctt	tatctctctt	ccttgcaaac	tacggccttg	tctgttgtct	tatgttcccta	33960
cagagattcc	tggtctcttt	tcaggaaacc	ttagctacac	ccatacggat	aacgatctga	34020
aaaccaagta	tacaacatat	cctactgtta	aaggaagctg	ggggaatgat	agtttcgctt	34080
tagaattcgg	tggaagagct	ccgatttgct	tagatgaaag	tgctctatct	gagcagtaca	34140
tgcccttcat	gaaattgcag	tttgtctatg	cacatcagga	agggtttaaa	gaacagggaa	34200
cagaagctcg	tgaatttgga	agtagccgtc	ttgtgaatct	tgccctacct	atcgggatcc	34260
gatttgataa	ggaatcagac	tgccaagatg	caacgtacaa	tctaactctt	ggttatactg	34320
tggtacttgt	tcgtagtaac	cccgaactga	cgacaacact	gcgaattagc	ggtgattctt	34380
ggaaaacttt	cggtagcaat	ttggcaagac	aagctttagt	ccttcgtgca	gggaaccatt	34440
tttgccttaa	ctcaaatttt	gaagccttta	gccaattttc	ttttgaattg	cgtgggtcat	34500
ctcgcaatta	caatgtagac	ttaggagcaa	aataccaatt	ctaattgcgtt	agctttggta	34560
aagagctcca	tacatcgaag	ggaaaagagc	ttttaagatt	tcttgaaggc	tcttttcgat	34620
ttcgatttcc	attttagtgt	tttgctaaaa	cactttctaa	tttttttctt	ttgttttcta	34680
cattgaaaaa	aagagagtta	cggcagctgt	aaagttttta	atattgctcc	ccttgttcca	34740
tttatgtagc	gttcagactt	tgacttaaaa	cgagggtgtc	atatgagatc	gtctttttcc	34800
ttgttattaa	tatcttcac	tctagccttt	cctctcttaa	tgagtgttcc	tcagatgctt	34860
gccgatctca	cattagggag	tcgtgacagt	tataatgggtg	atacaagcac	cacagaattt	34920
actcctaaag	cggcaacttc	tgatgctagt	ggcagcactt	atattctcga	tggggatgtc	34980
tcgataagcc	aagcagggaa	acaaacgagc	ttaaccacaa	gttgtttttc	taacaccgca	35040
ggaaatctta	ccttcttagg	gaacggattt	tctcttcatt	ttgacaatat	tatttcgtct	35100
actgttgcag	gtgttgttgt	tagcaatata	gcagcttctg	ggattacgaa	attctcagga	35160
ttttcaactc	ttcggatgct	tgacgtctct	aggaccacag	gtaaaggagc	cattaaaaatt	35220
accgatggct	tggtgtttga	gagtagtagg	aatcttgatc	ttaatgaaaa	tgccctagt	35280
gaaaatgggg	gagccatcaa	tacgaagact	ttgtctttga	ctgggagtac	gcggtttgta	35340
gcgttccttg	gcaatagctc	gtcgcaacaa	gggggagcga	tctatgcttc	tggtgactct	35400
gtgatttctg	agaatgcagg	aatcttgagc	ttcggaacaa	acagtgcgac	aacatcagga	35460
ggcgcgatct	ctgctgaagg	gaaccttggt	atctccaata	acaaaaatat	ccttttcgat	35520
ggctgcaaag	caactacaaa	tgggcgagct	attgattgta	acaaagcagg	ggcgaaccca	35580
gaccctactc	tgactctttc	aggaaatgag	agcctgcatt	ttctgaataa	cacagcagga	35640
aatagtggag	gtgcgattta	tacaaaaaaa	ttggtgttat	cctcaggacg	aggaggagtg	35700
ttattttcta	acaacaaagc	tgcaaatgct	actcctaaag	gaggggcaat	tgcgattcta	35760
gattctggag	agattagcat	ttctgcagat	ctcggaata	tcattttcga	gggcaatact	35820
acgagcacta	caggaagtcc	tgcgagtgtg	accagaaatg	ctatagatct	tgcatcgaat	35880
gcaaaatttt	taaactctcg	agcgactcgg	ggaaataaag	ttattttcta	tgatcctatc	35940
acgagctcag	gagctactga	taagctctct	ttgaataaag	ctgacgcagg	atctggaaat	36000
acctatgaag	gctacactgt	ttctctgga	gagaaactct	cagaagttaag	aaacctgaca	36060
atctgaagtc	tacattttaca	caggctgtag	agcttgctgc	agggtgcctta	gtattgaaag	36120
atggagtgcac	tgtagttgca	aatactataa	cgcaggctcga	gggatcgaaa	gtcgttatgg	36180
atggagggac	tacttttgag	gcaagcgctg	agggggctac	tctcaatggc	ctagccatta	36240
atatagattc	cttagatggg	acaaataaag	ctatcattaa	ggcgacggca	gcaagttaag	36300
atgttgccct	atcagggcct	atcatgcttg	tagatgctca	ggggaactat	tatgagcatc	36360
ataatctcag	tcaacagcag	gtctttgcct	taatagagct	ttctgcacaa	ggaacgatga	36420
ctactacaga	tatccccgat	accccaattc	taactactac	gaatcactat	ggtatcaagg	36480
gaactggaat	aattgttttg	gtcgacgatg	caactgcaaa	aacaaaaaat	gctaccttaa	36540
cttggaacta	aacaggatac	aagccgaatc	cagaacgtca	gggacctttg	gttcctaata	36600
gcctgtgggg	ttcttttgct	gatgtccgct	ccattcagag	cctcatggac	cggagcacia	36660
gttcgttatc	ttcgctcaaca	aatttggtgg	tatcaggaat	cgcggaactt	ttgcatgaag	36720
atcagaaagg	aaaccaacgt	agttatcgct	attctagcgc	gggttatgca	ttaggaggag	36780
gattcttcac	ggcttctgaa	aatttcttta	attttgcttt	ttgtcagctt	tttggctacg	36840
acaaggacca	tcttggtgct	aagaaccata	cccatgtata	tcgaggggca	atgagttacc	36900
gacacctcgg	agagtctaag	accctcgcta	agattttgtc	aggaaattct	gactccctac	36960
cttttgctct	caatgctcgg	tttgcttatg	gccataccga	caataacatg	accacaaagt	37020
acactggcta	ttctcctggt	aagggaagct	ggggaaatga	tgcttctcgt	atagaatgtg	37080
gaggagctat	cccggtagtt	gcttcaggac	gtcgggtctg	ggtggatacc	cacacgccat	37140
ttctaaacct	agagatgata	tatgcacatc	agaatgactt	taaggaaaac	ggcacagaag	37200
gccgttcttt	ccaaagtga	gacctcttca	atctagcggg	tcctgtaggg	ataaaaattg	37260
agaaattctc	cgataagtct	acgtatgata	tctccatagc	ttacgttccc	gatgtgattc	37320
gtaatgatcc	aggctgcacg	acaactctta	tggtttcttg	ggattcttgg	tcgacatgtg	37380
gtacaagctt	gtctagacaa	gctcttcttg	tacgtgctgg	aaatcatcat	gcctttgctt	37440
caaactttga	agttttcagt	cagtttgaag	tcgagttgct	agggtcttct	cgtagctatg	37500
ctatcgatct	tgagggaaga	ttcggttttt	aatcctaagt	tttccaacga	gatagcatca	37560
gggtaagcca	gggctctatg	taagagattt	catagagccc	tctctttgtc	ttgctttttg	37620
tatttttatt	ttatatctcg	tgaatccggt	gttccaatgt	tcgaaaggta	tcctagatga	37680

gatttgctgtt	gtcttgcct	atgcttttta	tagctgcatg	tgccctcattt	tttggctttc	37740
aggaagaaat	gcaaggcaga	aatacataat	ctcttgatgc	aaatgcttct	agtctagggg	37800
aacttttttc	tatttctacg	aaggagtggt	cttgcttaga	actccatagg	gagatcgac	37860
gctaaatatg	agaatataat	atgaagactt	cagtttctat	gttggtggcc	ctgctttgct	37920
cgggggctag	ctctattgta	ctccatgccg	caaccactcc	actaaatcct	gaagatgggt	37980
ttattgggga	gggcaataca	aatacttttt	ctccgaaatc	tacaacggat	gctgcaggaa	38040
ctacctactc	tctcacagga	gaggttctgt	atatagatcc	ggggaaagg	ggttcaatta	38100
caggaacttg	ctttgtagaa	actgctggcg	atcttacatt	tttaggtaat	ggaaataccc	38160
taaagtccct	gtcggtagat	gcaggtgcta	atatcgcggt	tgctcatgta	caaggaagta	38220
agaatttaag	cttcacagat	ttcctttctc	tggtgatcac	agaatctcca	aaatccgctg	38280
ttactacagg	aaaaggtagc	ctagtcaagt	taggtgcagt	ccaactgcaa	gataataaca	38340
ctctagtctt	tacaagcaat	gcctctgtcg	aagatgggtg	cgtgattaaa	ggaaactcct	38400
gcttgattca	gggaatcaaa	aatagtgcga	tttttggaca	aaatacatct	tcgaaaaaag	38460
gaggggcat	ctccacgact	caaggactta	ccatagagaa	taacttaggg	acgctaaagt	38520
tcaatgaaaa	caaagcagtg	acctcaggag	gcgccttaga	tttaggagcc	gcgtctacat	38580
tcaactgcga	ccatgagttg	atattttcac	aaaataagac	ttctgggaat	gctgcaaatg	38640
gcgagccat	aaattgtcga	ggggacctta	ctttactga	taacacttct	ttgtacttc	38700
aagaaaatag	cacaatgcag	gatggtggag	catttgtag	cacaggaacc	ataagcatta	38760
ccggtagtga	ttctatcaat	gtgataggaa	atacttcagg	acaaaaagga	ggagcgattt	38820
ctgcagcttc	tctcāāgaft	ttgggagggc	agggagggcg	tctcttttct	aataacgtag	38880
tgactcatgc	caccctctca	ggaggtgcca	tttttatcaa	cacaggagga	tccttgcagc	38940
tcttcaactca	aggaggggat	atcgtattcg	aggggaatca	ggctactaca	acagctccaa	39000
atgctaccac	taagagaaat	gtaattcacc	tcgagagcac	cgcgaaagtg	acgggacttg	39060
ctgcaagtca	aggtaacgct	atctatttct	atgatcccat	taccaccaac	gatacgggag	39120
caagcgataa	cttacgtatc	aatgaggtca	gtgc aaatca	aaagctctcg	ggatctatag	39180
tattttcttg	agagagattg	tcgacagcag	aaagctatagc	tgaaaatctt	acttcgagga	39240
tcaaccagcc	tgctacttta	gtagagggga	gcttagtact	taaacaggga	gtgaccttga	39300
tcacacaggg	attctcgcag	gagccagaaat	ccacgcttct	tttggatctg	gggacctcat	39360
tataagcttc	tacagaagat	attgtcatca	caaatttatc	tataaatgcc	gataccattt	39420
acggaaagaa	tcctatcaat	attgtagctt	cagcagcgaa	taagaacatt	accctaacag	39480
gaaccttaag	acttgtaaat	gcagatggag	ctttctatga	gaaccatacc	ttgcaagact	39540
ctcaagacta	tagcttttga	aagttatctc	caggagcggg	agggactata	attactcaag	39600
atgcttctca	gaagcctctt	gaagtagctc	cttctagacc	acattatggc	tatcaaggac	39660
attggaatgt	gcaagtcac	ccaggaacgg	gaactcaacc	gagccaggca	aatttagaat	39720
gggtgcggac	aggatacctt	ccgaatcccg	aacggcaagg	atcttttagt	cccaatagcc	39780
tgtgggggtc	ttttgttgat	cagcgtgcta	tccaagaaat	catggtaaat	agtagccaaa	39840
tcttatgtca	ggaacgggga	gtctggggag	ctggaattgc	taatttccta	catagagata	39900
aaattaatga	gcaccgctat	cgccatagcg	gtgtcggtta	tcttggtgga	gttgccactc	39960
atgctttttc	tgatgctacg	ataaatgcgg	ctttttgcca	gctcttcagt	agagataaag	40020
actacgtagt	atccaaaaat	catggaacta	gctactcagg	ggctcgattt	cttgaggata	40080
ccctagagtt	tagaagtcca	cagggattct	atactgatag	ctcctcagaa	gcttgctgta	40140
accaagtcgt	cactatagat	atgcagttgt	cttacagcca	tagaaataat	gatatgaaaa	40200
ccaaatacac	gacatatcca	gaagctcagg	gatcttgggc	aaatgatgtt	tttggctctg	40260
agtttggagc	gactacatac	tactacccta	acagtaactt	tttatttgat	tactactctc	40320
cgtttctcag	gctgcagtg	acctatgctc	accaggaaga	cttcaaagag	acaggaggtg	40380
agggttcgtca	ctttactagc	ggagatcttt	tcaatttagc	agttcctatt	ggcgtgaagt	40440
ttgagagatt	ttcagactgt	aaaaggggat	cttatgaact	tacctttgct	tatgttctctg	40500
atgtgattcg	caaagatccc	aagagcacgg	caacattggc	tagtggagct	acgtggagca	40560
cccacggaaa	caatctctcc	agacaaggat	tacaactgcy	tttagggaac	cactgtctca	40620
taaactcctg	aattgaggtg	ttcagtcacg	gagctattga	attgcgggga	tcctctcgta	40680
attataacat	caatctcggg	ggtaaatacc	gattttaata	gggaactgag	agttccttat	40740
tgtagagagt	atttacaagg	attttgagac	gaaagagatt	tcttggttga	ggtatctctc	40800
cacagggtct	agttcaattt	ctatagttca	tgggggttct	ttttttataa	agaagaaacc	40860
ccatgtctga	cgagacctca	cctggatcta	ttgcattctc	tatggtaagg	gatccatgac	40920
ttgacacagg	aggttcattc	tcatgtctaa	gtcagaggtt	agaagggagg	ttttttaagg	40980
tttgctcgagc	tttaagaaga	agaaaaatcg	actatctgct	tctcggcgtt	catacaccoc	41040
atagagctgc	caatgttcga	agatcttcgt	ccctagaatc	atctgggtatt	ctaggtagtt	41100
cggagtgtcc	tgcgatgcca	gccatagcgt	aaggataagc	ggtaattcca	acagggatga	41160
ggtcgtacaa	ttaatttccc	taaaatgaga	ttcctatgat	cagagagagg	ggagtctaaa	41220
agctgggtcaa	tgggacggct	gacatctaaa	atgaagttct	ccctgtcaca	cttaatcagg	41280
ctgtatttgc	ttctatgcag	ggattctaga	gtcatagcca	cattgtcatt	tccgatccac	41340
tcccaacgta	tgttcatgtg	atcccaacag	tgctttttcc	aaatccattc	agcatctaa	41400
gagactgtat	ttttctttcc	aaaaggtaga	gatagctcgc	atgcagtttt	gggaaacgtg	41460
ggtttgcttt	ctgtattgct	caagatgtgg	gtagtcacaca	gcttcgcatg	gattctcggg	41520

aatcggagggt	tagtcttact	cagtaccgag	gtatctatac	ccgctttcag	aagggtttaag	41580
gagtgaagg	catcttgaat	ggaaaagata	taatgatctt	cattcttagc	tagaggacga	41640
gtctctgtaa	tgaaggtaac	gaacggctct	ataatatggc	gtctttgaat	gtaggactta	41700
tgtaatagaa	agcgataatc	aagttgtagc	ttcgcggaaa	gctgactatg	gcgcgaggag	41760
atctcaggaa	catcgctata	gtaaatcaga	gaactcccta	gggtggagga	gagcgttccct	41820
ataggtagag	gcacagtttt	atggagctta	gggcgcgcag	caagacgtag	tgaagagaaa	41880
ttctcgccaa	cgatatgata	gctaaaagca	aagtttaaat	acccacattc	tacgatgttt	41940
tcaaggtaga	ctcccgattt	ataaatagaa	atcgggtact	gccttaatgt	taaataagggt	42000
agctcttggg	tggcattttt	gaaagagttt	accttaacag	aagaggtgag	atacccttca	42060
aaatagttgt	cattccaagt	gcaatcgaca	cgtgtggggc	ctgtattttt	caacatgaag	42120
ttgttgggga	aaatgtcagc	aacagttttc	caactatcgc	tgagatggta	ttctccgaa	42180
aaatttacat	gcttatgcgt	gaagcagaaa	tctccgtgta	ggcgatagcg	atcatgagct	42240
tctgccaat	cgatagcaag	gcggtgggca	taatagcttt	tcatattgaa	gacattctca	42300
ggaacctgct	tctgagaaca	atggaggttg	aatcccatgc	cgacgccatg	cttgaaaaag	42360
ctatccaaga	aaaaatgtoga	ggagaaatgc	ttcctagaaa	tcggcgagta	gctcatcccc	42420
aaataggatc	ccagaaatcc	tctgtttcct	cctcgaaagt	ttatcggagg	cttagggatc	42480
tccataggca	tgatagaaaa	tggaggtgaag	aaaagtatcg	gaatgcgaca	cacccttaat	42540
gttgccttcc	ctatagaaag	aagactatct	gaagataatt	ccaggtaatc	tccggagagg	42600
cacaggtctt	ttttgggacc	ctcggaggta	gagatatatc	ccttccgaat	gactatgggt	42660
tctgggggta	gagtgtcat	agacccccct	agaaaccaag	gatacatcgc	gaatcttcca	42720
ttagtaagaa	gacaagagtc	tgtatcttcg	taatactcta	ggtaatcaca	aactaggggt	42780
tttgccctat	agttcaccat	aacattgccca	tgtgcgacaa	gcttcagggt	ttgaccaca	42840
gtattttcta	catacacttt	attggcttgt	atccgcagggt	tgttatggat	attcaatacc	42900
ccatcttcca	tgggtcacaat	cccagaaaca	ctcttaaagt	gactaagata	ggagtttttc	42960
tttttcacag	cctcttgatg	agtc aaagca	tcagctgagg	aacccataag	aacaaaggaa	43020
gctagaaata	agaagcaacg	tttcataaga	cgtaggttgg	ggttactcca	caatttttat	43080
gagtaagcct	gcaaggactg	ggaaattttt	tgcactcctt	tccgtcatca	gttgatcaa	43140
taaacggata	tcttcggaag	acttcgaggt	ggctagtgtc	tctagaatat	ccaacatgag	43200
cttcgtacgg	ctttctgggg	tgacctgata	acgtagatag	ggcatgctgg	gatgggggtc	43260
ttggttttcc	gtgtccacaa	ataacaaggt	ttcctgaatt	agcttttttg	cataatcatg	43320
gagagaacgt	tttttttcag	gatcttttgt	gagattataa	atagcaagat	ctgcataggc	43380
gcggatgata	ggttctccag	gaagcttcgc	agcttggaaa	agtagatcta	aggcttctctg	43440
atgtgaggtg	tgacttaaaa	aagaaatcgc	agtagtgcca	agctgagttt	tctgactcgc	43500
caaaagctta	taaatacagg	ggaggtgaag	ttcttttaggt	aggcgggaag	gaaacgtaag	43560
gatctgctct	tcaagacctc	gggttgtgga	gagcaacctt	tccctctcct	ggggatcttg	43620
agggactatg	atgttcaccc	gcttccaatt	ttgtaaagta	cgcccttag	agaaactcaa	43680
ggctagagtc	tcattataat	gtgggtggac	aagcctttcg	gtaatgtatt	ccagtagttt	43740
aggggtgtca	caccctaact	ctaagagagc	ttaaagctaca	ttcaacttgc	ttcgtgttcc	43800
ttagttttta	ggaatatcgg	cagggaatc	ggaatcccta	tctcagaggg	tagatgccgt	43860
aaggcataca	gggctcaggg	ccgctcctca	agtgtctgct	tttttatcac	gggaagagcg	43920
tctcttctct	tcccaaaagc	aattaaagct	tgagctgctg	ctaaagtac	atccacatca	43980
ggcttctgca	attgtctttt	tattattgtag	tagctctgac	catccttaag	cttccctaaa	44040
gcataaagaa	tagcttcttg	atcttgagga	gacgcactcg	ttagcaaat	cctaagtgtc	44100
ggaagaaagc	gtttttgttg	gtattctccg	atctgcaaag	ctgtggcact	ccgaatcgcg	44160
cttttcttgg	cagctaagag	atcccgaata	taagcatcag	attcttcagt	ctccaagcgt	44220
aggaatatgg	ccgcagatag	gcattggatt	tcttcgggaa	gcttatgaat	gaaagaatgt	44280
agatgatcaa	tgacttttagt	gttcttcaaa	ttagcaagtc	tataggcggc	ttctaagcgg	44340
atgacaggat	agggagatgc	taaagcttta	aacagtaagt	cgtcagaagt	tttcccaaga	44400
tgctctgaga	ctgccgataa	aaccagtagc	tgctgcaggg	ggctctgagt	ttccatagct	44460
tgggagagca	cgtccaaggc	ttctgaagat	cccgccaggc	ctgctccaat	gatgggtgct	44520
tttctagttt	gcggatctga	ggagtggatg	ctttgtctga	gatagtcttc	tccgattttt	44580
cttaaaacga	agaagtcag	atcacgtag	gcatctagag	cttccagata	tggtgctaag	44640
gcctgctgtg	tagattgcgt	acttatataa	aggatcttat	gacctacaga	ctcagggaat	44700
ttagcaacaa	gagaaatggg	aagactacac	aataaaagtc	caaagagagt	tagatggaat	44760
agtcccatag	atcgatgttc	aactcctcta	gcaagtattt	caatgtttgg	atagggagac	44820
cttgaacatt	ataaacacat	ccatggacct	ttttcaaaat	caagccacca	tggcaaacgt	44880
cataagcgcc	acaattattt	aatgttccta	cagtgtcgat	ataagactct	atgcggtgat	44940
caggaaatcat	agtaagtga	atctgagaag	tctctgaccc	tgtgaggagt	tttcccttat	45000
gtaatacggc	aatactcgtg	accacatcat	gcgtctgatt	cctcaaggtc	tttaacatct	45060
ggatagcggn	tgctttgnct	tgaggttttg	tgaaaatacg	gccatcgtaa	gaaacaatag	45120
tatcgccagt	gaggataata	cagtcacaag	gcgaatgtag	ctcagaaact	gcataggcct	45180
tttgtgcggc	aagttcttgt	gtataggcta	taggatcccc	agagtagctg	actttactct	45240
catcaaaatt	tgaaggaaatg	acagtaaagg	gaacacgaaa	tttttctaaa	ataaaattttc	45300
ttcttggcga	agaagaccct	aaaactaaag	gaagggaat	agaataaaag	ctcctcgtgt	45360